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Abp98904 Human mol Adc31420 Human nov

ALIGNMENTS

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RESULT 1
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                                                                                                                                                                                                                                                                                                                              The present sequence is the protein sequence of Streptococcus sobrinus glucosyltransferase-I (GTF-I). Peptide fragments of GTF-I, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II protein-binding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal collections. The compositions are used in a claimed method of glucosyltransferase. The compositions are used in a claimed method of glucosyltransferase. The compositions are used in a claimed method of
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08-AUG-2002; 2002US-0402483P
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                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                             eliciting production of an antibody in a mammal Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 14; 49pp; English.
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N-PSDB; AAQ37760.
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                                                WPI; 2002-448885/48.
                                                                                                                                                                                                     04-OCT-2000; 2000JP-00304889
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                                                                                                                                                       04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                 transferase-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPSYSFARAHDSEVQDIIRDII 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                      dental caries; water insoluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                       2000JP-00304889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                      immunotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108; DB 2;
Pred. No. 3.6e-09;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                              glucan synthetase; anti-caries;
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Anti-caries agent

composed of a monoclonal antibody against

an inhibitory

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a monoclonal antibody against dental caries and an anti-caries agent composed of a monoclonal antibody produced by Streptococcus mutans, particularly mouse-hybridoma MHP126 (FERM P-17567), against an enzyme having inhibitive activity against water insoluble glucan synthetase of glucosyl transferase-B. The monoclonal antibody specifically inhibits water insoluble glucan synthetase of Streptococcus mutans produced glucosyl transferase-B and is used in the immunotherapy of dental caries. This transferase-B and is used in the immunotherapy of dental caries. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; glucosyl t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme against water insoluble glucan synthetase of glucosyl transferase- {\tt B} (GTF-{\tt B}) of Streptococcus mutans.
                                                                                                                                an anti-caries agent composed of a monoclonal antibody produced by Streptococcus mutans, particularly mouse-hybridoma MHP126 (FERM P-17566) or mouse-hybridoma MHP136 (FERM P-17567), against an enzyme having
                                                                                                                                                                                                                                                        Anti-caries agent composed of a monoclonal antibody against an inhibitory enzyme against water insoluble glucan synthetase of glucosyl transferase-B (GTF-B) of Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2002114709-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU79284 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 17-19; 28pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000; 2000JP-00304889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2002
                                                               inhibitive activity against water insoluble glucan synthetase of glucosyl transferase-B. The monoclonal antibody specifically inhibits water insoluble glucan synthetase of Streptococcus mutans produced glucosyl transferase-B and is used in the immunotherapy of dental caries. This
                                                                                                                                                                         The invention relates to a monoclonal antibody against dental caries and an anti-caries agent composed of a monoclonal antibody produced by
                                                                                                                                                                                                                        Claim 3; Page 13-16; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                               WPI; 2002-448885/48
                                                                                                                                                                                                                                                                                                                                                                 (UYNI-) UNIV NIPPON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dental caries; water insoluble glucan synthetase; anti-caries; transferase-B; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPSYSFIRAHDSEVODLIRDII 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutans monoclonal antibody-related protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a Streptococcus mutans monoclonal antibody-related
                                                a Streptococcus mutans monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1476
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Pred. No. 6.9e-09;
0; Mismatches 1
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Sequence 1476 AA

sequence represents

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Query Match
Best Local S
Matches 21
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07-JUN-1995;
07-JUN-1995;
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16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
                                                                                                                                                                     Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in pape manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                            Glucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU98028 standard;
                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                        WPI; 2002-414332/44
                                                                                                                                                                                                                                                                                                         19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                    US2002031826-A1
                                                                                                                                                                                                                                                                                                                                                 Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                              amyloplast; vacuole;
                                                                                                                                                                                                                                                                                                                                                                     coating composition;

    mutans glucosyltransferase

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                                                                                                                                                                                                                                                                                                                                                                                                                      AAU98028;
                                                                                                                                                        Disclosure; Page 30-33; 44pp; English.
                                                                                                                                                                                                                                                                                                                      14-MAR-2002.
                                                                                                                                                                                                                                    (NICH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
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                                                                                                                                                                                                                                                95US-00478704.
95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 1375
                                                                                                                                                                                                                                                                                                                                                                     GTFC; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.5%;
                                                                                                                                                                                                                                                                                                                                                               paper
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                                                                                                                                                                                                                                                                                                                                                                        molecule;
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chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. Glucans are useful as substitutes for and additions to modified starch and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence represents GTFC

conditions to produce a regenerated plant and inducing expression of the polymucleotide for a time sufficient to produce the glucan in the regenerated plant, where the vector contains a transit sequence from ribulose biphosphate carboxylase small subunit, waxy, brittle-1 and

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Query Match Best Local S Matches 20

Similarity

90.9**%;** 90.9**%**;

Score 100; Pred. No. 7.

DB 5;

Length 1375;

Conservative

۳.

Mismatches

Indels

0; Gaps

0,

Sequence 1375 AA;

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The invention relates to a monoclonal antibody against dental caries and an anti-caries agent composed of a monoclonal antibody produced by streptococcus mutans, particularly mouse-hybridoma MHP126 (FERM P-17567), against an enzyme having inhibitive activity against water insoluble glucan synthetase of glucosyl transferase-B. The monoclonal antibody specifically inhibits water insoluble glucan synthetase of Streptococcus mutans produced glucosyl transferase-B and is used in the immunotherapy of dental caries. This transferase-B and is used in the immunotherapy of dental caries. This
                                                                                                                                                                                                                                              Anti-caries agent composed of a monoclonal antibody against an inhibitory enzyme against water insoluble glucan synthetase of glucosyl transferase-B (GTF-B) of Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000; 2000JP-00304889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP2002114709-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucosyl transferase-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; dental caries; water insoluble glucan synthetase; anti-caries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans monoclonal antibody-related protein #5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU79288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU79288 standard; protein; 1375
                                                                                                                                                                                                                                                                                                              WPI; 2002-448885/48.
                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                             (UYNI-) UNIV NIPPON.
                                                  represents
                                                                                                                                                                                                                 Page 22-25; 28pp; Japaneве.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutans
                                                    a Streptococcus mutans monoclonal antibody-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy.
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Query Match

90.9%;

Score 100;

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Length 1375;

RESULT 8
AAU98031
ID AAU9
XX
AC AAU9
XX

AAU98031 standard; protein; 1475 AA

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AAU98031

Sequence

1375

8

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RESULT 7
ADD93655
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                                                      Matches
                                                                   Query Match
Best Local
                                                                                                                                    The present sequence is the protein sequence of Streptococcus mutans glucosyltransferase-C (GTF-C). Peptide fragments of GTF-C, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MMC) class II proteinbinding peptide from S. mutants glucan binding protein-B (GDpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucosyltransferase; enzyme; vaccine; anticaries; epitope; immunogen
                                                                                                                                                                                                                                                                                                                                                         Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans glucosyltransferase-C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD93655 standard;
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08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2003; 2003WO-US006962.
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                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 13; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-845091/78.
                                                                                                               Sequence 1375 AA;
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578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPSYSFIRAHDSEVQDLIRNII 599
                VPSYSFARAHDSEVQDLIRDII 22
 VPSYSFIRAHDSEVQDLIRNII 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taubman MA;
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                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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1; Mismatches 1
                                                      Score 100; DB 7;
Pred. No. 7.2e-08;
1; Mismatches 1
                                                                                    Length 1375;
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                                                            Indels
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27-AUG-2002

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entry

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CC complementary polynucleotide, a ribonucleic acid sequence encoding the CC gfF mutant, an axpression cassette comprising the polynucleotide operably CI linked to a promoter, a vector comprising the polynucleotide operably CC linked to a promoter, a vector comprising the polynucleotide operably CC cell introduced with the vector, a transgenic plant, a paper sizing and/or coaring composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GFF, wild type or starch, a latex, CC thermoplastic molecule or their combinations or glucan and starch where CC deficient in starch biosynthesis, transformed with a gene encoding a glucan transformed with a gene encoding a glucan transformed with a gene encoding a CC glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC comprising the glucan (paper sizing/coating agent). The vector is useful comprising the glucan in a plant. The method comprises transforming a CC plant cell with the vector, growing the plant cell under plant growing CC conditions to produce a regenerated plant and inducing expression of the CC conditions to produce a regenerated plant and inducing expression of the CC comprision of the vector contains a transit sequence from CC comprision of the vector contains a transit sequence from CC comprision of the vector contains a transit sequence from CC comprision of the vector contains a transit sequence from CC contains are useful as substitutes for and additions to modified starch conditions to modified star
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from I448V, D457N, D567T, R1014T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K, D567T/D571K, D567T/D571K/R1014T, I169A/Y170A/Y171A, and K779Q or a I448V/D457N/D567T/D571K/K779Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D, N471D/T589D, and N471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 36; Page; 44pp; English
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07-JUN-1995;
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require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and
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98US-00008172.
98US-00009620.
98US-00210361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTFB mutant D457N
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latexes i
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Best Local S
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07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          properties and impart gloss to the paper during coating step. The presequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using the GTFB sequence appearing claim 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 environmentally friendly. Moreover,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU98040 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1475
                  The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from I448V, D457N, D567T, R1014T, D457N/D567T, D457N/D571K, D567T/D571K, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amyloplast; vacuole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-2002
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                                                                                                                                                                                                                                         Glucosyltransferase B or D protein as substitutes for and additions to manufacture, comprises mutations in
                                                                                                                                                                                                                                                                                                                                                                              Nichols
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                                                                                                                                                                                                  Claim 36; Page; 44pp; English
                                                                                                                                                                                                                                                                                                                                WPI; 2002-414332/44
                                                                                                                                                                                                                                                                                                                                                                                                                       (NICH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
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95US-00482711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; DB 5; LC
Pred. No. 1.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant K779Q.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutant;
                                                                                                                                                                                                                                                  positions.
                                                                                                                                                                                                                                                                       starch and
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latexes in pape
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complementary polynucleotide,

a ribonucleic acid sequence

encoding

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RESULT 10
AAU98033
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PRRRACE XXX
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
                                                                                                                                                                           Glucosyltransferase; coating composition; amyloplast; vacuole;
                                                                                                                                                                                                                                                                              AAU98033 standard; protein; 1475 AA
                                               19-DEC-2000;
                                                                   14-MAR-2002
                                                                                       US2002031826-A1
                                                                                                               Ney Location/Qualifiers Misc-difference 1014
                                                                                                                                                Synthetic
                                                                                                                                                          Streptococcus
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                                                                                                                                                                                                                   glucosyltransferase GTFB mutant K1014T.
                                                  2000US-00740274
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                           mutans
         95US-00482711.
95US-00485243.
                              95US-00478704
                                                                                                          /note= "Wild-type Lys substituted by
                                                                                                                                                                             GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule; paper manufacture; mutant; mutein.
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AAU98030
ID AAU9
XX
AC AAU9
XX
DT 27-2

standard; protein; 1475

27-AUG-2002 AAU98030; AAU98030

(first entry)

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Matches Query Match

μ

VPSYSFARAHDSEVQDLIRDII 22

VPSYSFIRAHDSEVQDLIADII 573

Local

Similarity

90.0%;

Score Pred. 0;

Length 1475;

0,

Gaps

0

Mismatches 99; I В 2e-07; υ U

Conservative

RESULT 11

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linked to a promoter, a vector comprising the polynucleotide operably cell introduced with the vector, a transgenic plant comprising the vector, as a seed or tuber from the transgenic plant comprising the coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, child the plant transformed with a gene encoding a glucan is produced in the amyloplast and/or vacuole or a maize line child the plant and spaper comprising the glucan in a plant. The method comprises transforming a glucan in a plant transformed a paper gollutions to produce a regenerated plant and inducing expression of the plant cell under plant growing conditions to produce a transforming a transforming a conditions to produce a transforming a chlorophyll AB binding protein to produce the glucan in the conditions to suspen seet. Cc glucans are useful as substitutes for and additions to modified starch cc amountacture utilising the glucan produced by GTP, which utilises biologically produced input materials, is more cost-effective and cc environmentally friendly. Moreover, glucans also exhibit thermoplastic cromoperties and impart gloss to the paper during coating step. The present sequence represents a GTPB mutant of the invention. Note: The present consing the GTPS sequence appearing as AAU98027 and the information in cc claims the function in call the filter the produced by the indexer using the GTPS sequence appearing as AAU98027 and
16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 36; Page; 44pp; English.
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paper

CC 1448V/0457N/D567T/D57Tk/K779Q/KU14T, Its PAK 11 VAK, 11 VAK, 12 VAK, 12 VAK, 12 VAK, 12 VAK, 13 VAK, 13 VAK, 13 VAK, 14 VAK, 14 VAK, 15 VAK, 16 VAK, 16 VAK, 16 VAK, 16 VAK, 17 VAK, 18 VAK The invention an isolated protein comprising a glucosyltransferase B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K, D47N/D457N/D571K, D47N/D47N/D47N/D571K, D47N/D47N/D47N/D571K, D47N/D47N/D47N/D57N/D57N/K1014T, Y169N/Y170N/Y171N, and K779Q Sequence 1475 Å 90 or a (GTF)

Best Local Similarity Matches 20; Conser

Conservative

0,

90.0%;

Score 99; DB 5; Le Pred. No. 1.2e-07;

Length 1475

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Query Match

Sequence 1475

A,

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CC The invention an isolated protein comprising a glucosyltransferase (GTF) CC B polypeptide having changes at position from I448V, D457N, D567T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K, D567T/D457NK/D14T, CC I448V/D457N/D567T/D571K/E044T, F0567T/D571K/E044T, CC I448V/D457N/D567T/D571K/E044T, And K779Q or a CC GTF D501ypeptide having changes at positions from T589D, T589E, N471D, CC N471D/T589E, Also included are a glucan produced by the CC GTF mutant, an isolated polymucleotide which encodes P1 or P2, or its CC complementary polymucleotide, a ribonucletic acid sequence encoding the CC GTF mutant, an expression casette comprising the expression casette, host CC cell introduced with the vector, a transgenic plant comprising the conting composition comprising a glucan produced in a plant transformed CC wettor, a seed or tuber from the transgenic plant, a paper sizing and/or coating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTF, wild type or, starch, a latex, cot the glucan is produced in the amyloplast and/or vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a CC glucosyltransferase B or D enzyme, wild-type or mutant and a paper comprising the glucan in a plant transforming a plant cell with the vector, growing the plant cell under plant growing conditions to produce a regenerated plant and inducing expression of the CC polynucleotide for a time sufficient to produce the glucan in the comprise transforming a growing the plant cell under plant, and glucan cell the plant cell under plant, and glucan in the myloplast and inducing expression of the complexity and the amyloplast of positions to growing the glucan produce a transgenic plant, and glucan cell plant, and glucan cell plant, and glucan cell plant, and glucan produced by GTF. Which waxy, brittle-1 and cell plant as substitutes for and additions to modified starch and inducing expression cell plant cell plant as more cost-effective and colorable pla
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The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K/K1014T, I1648V/D457N/D57TK/T90Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D, M471D/T589D, and N471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the GTF mutant, an expression cassette comprising the polynucleotide operably
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Synthetic.
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20-JAN-1998;
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98US-00009620.
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latexes in pape
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Nichols SE

Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in paper manufacture, comprises mutations in specific positions.

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Congrished in starch biosynthesis, transformed with a gene encoding a glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC comprising the glucan in a plant. The method comprises transforming a CC plant cell with the vector, growing the plant cell under plant growing CC conditions to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the CC polynucleotide for a time sufficient to produce the glucan in the CC risulose biphosphate carboxylase small subunit, waxy, brittle-1 and CC chlorophyll AB binding protein to porduce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. CC glucans are useful as substitutes for and additions to modified starch cC and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper CC manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and cc environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in
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Matches
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                                                        07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
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                                                                                                                                                                                                                                                                                                                              Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                  coating composition;
amvloplast; vacuole;
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                    (NICH/) NICHOLS
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95US-00485243.
95US-00007999.
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98US-00210361.
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Pred. No. 1.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 14 ADD93654

ADD93654 standard; protein; 1475

XXXXXXXXXXXXXXX

29-JAN-2004

(first entry)

Streptococcus mutans glucosyltransferase-B.

Streptococcus mutans

Glucosyltransferase; enzyme;

vaccine; anticaries; epitope; immunogen

WO2003075845-A2

Ś 무

1 VPSYSFARAHDSEVQDLIRDII 22

552

VPSYSFIRAHDSEVQDLIADII 573

Query Match Best Local S Matches 20

Similarity

90.0%;

Score 99; DB 5; Le Pred. No. 1.2e-07; 0; Mismatches 2;

Length 1475

0,

Gaps

0

Conservative

Sequence 1475 AA;

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The invention an isolated protein comprising a glucosyltransferase (GTF) CC Hydry, D457N,D567T, D457N/D571K, D567T/D571K,D57T/D571K,D567T/D57TK,D457T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57T/D57TK,D57TK,D57T/D57TK,D57T/D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57TK,D57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 21-25; 44pp; English.
                                                         impart gloss
sents GTFB
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RESULT 15
AAU98035
THE PROOF OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the protein sequence of Streptococcus mutans glucosyltransferase-B (GTF-B). Peptide fragments of GTF-B, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II protein-binding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 12-13; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2003; 2003WO-US006962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. mutans glucosyltransferase GTFB mutant D457N/D571K.
                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                         coating com
amyloplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU98035 standard; protein; 1475 AA
                           19-DEC-2000; 2000US-00740274
                                                                                                                                       US2002031826-A1
                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VPSYSFARAHDSEVQDLIRDII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                         composition; ast; vacuole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPSYSFIRAHDSEVQDLIADII 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                 571
                                                                                                                                                                                                /note= "Wild-type Asp substituted by Lys"
                                                                                                                                                                                                                                                         note= "Wild-type Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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RESULT 16
AAU98034
ID AAU98

AAU98034 standard; protein; 1475

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음 성

552

VPSYSFIRAHDSEVQDLIAKII 573

1 VPSYSFARAHDSEVQDLIRDII 22

Query Match Best Local : Matches 1

19;

Conservative

Score Pred. 0; Mis

Mismatches

92;

DB 5; 1.9e-06

Length 1475;

0

Gaps

0

Similarity

86.4%;

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PR 07-UNN-1995; 95US-00442771.
PR 07-UNN-1995; 95US-0048271.
PR 16-ANN-1999; 95US-0048272.
PR 16-ANN-1999; 95US-00008729.
PR 16-ANN-1999; 95US-00008729.
PR 16-ANN-1999; 95US-00009729.
PR 11-DEC-1999; 95US-00009729.
PR
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CC The invention an isolated protein comprising a glucosyltransferase (GTF) CC B polypeptide having changes at position from I448V, D457N, D567T, CC I448V,D457N,D567T,D571K/K1014T, CC I448V/D457N/D567T,D571K/K792/K104T, D567T/D571K/K7104T, CC GTF D polypeptide having changes at positions from T589D, T589E, N471D, CC GTF D polypeptide having changes at positions from T589D, T589E, N471D, CC GTF mutant, an isolated polymucleotide which encodes P1 or P2, or its complementary polymucleotide, a ribonucleic acid sequence encoding the CC GTF mutant, an expression cassette comprising the polymucleotide operably comprising the produced by the cell introduced with the vector comprising the expression cassette, host cell introduced in the vector, a transgenic plant, a paper sizing and/or vector, a seed or tuber from the transgenic plant, a paper sizing and/or coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, with a gene encoding the mutant GTF, wild type or, starch, a latex, cc the glucan is produced in the anyloplast and/or vacuole or a maize line deficient in starch biosynthesis, transformed with a gene encoding a glucan (paper sizing/coating agent). The vector is useful for producing a glucan in a plant. The method comprising the vector is produced in the vector starch and a paper comprising the vector spanerated plant and inducing expression of the polymucleotide for a time sufficient to produce the glucan in the comprises transforming a transit sequence from the polymucleotide for a time sufficient to produce the glucan in the comprise to produce a regenerated plant, where the vector contains a transit sequence from chlorosphyll AB binding protein to produce a transgenic plant, and glucan in the produce of the plant, and glucan in the amyloplast of potato or the vacuole of sugar beet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S. mutans glucosyltransferase GTFB mutant D457N/D567T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amyloplast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as substitutes for and additions manufacture, comprises mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 36; Page; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-414332/44.
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95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
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567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ħ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                paper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermoplastic
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latexes in pape
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RESULT 17
AAU98032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTP, which utilises biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in claim 36
                                                                                                                                                                 07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1475
                                                                                                                                                                                                                                                                                                                                                        Streptococcus Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                S. mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU98032 standard; protein;
                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                       14-MAR-2002.
                                                                                                                                                                                                                                                                                             US2002031826-A1.
                                                                                                                                                                                                                                                                                                                                                                                       amyloplast;
                                                                                                                                                                                                                                                                                                                                                                                                  Glucosyltransferase; coating composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU98032;
                                                                                                                          Nichols
                                                                                                                                                                                                                                                     19-DEC-2000;
                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                      Glucosyltransferase B o as substitutes for and
                                                                                                     WPI; 2002-414332/44.
                                                                                                                                               (NICH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552
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                                                                                                                                                                                                                                                                                                                                                                                                                                glucosyltransferase GTFB mutant D567T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                         vacuole;
                                                                                                                                                                                                                                                     2000US-00740274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                    mutans
                                                                                                                                                                  95US-00478704.
95US-00482711.
95US-00485243.
98US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 567
                                                                                                                                               Ø
                                                                                                                                                                                                                                                                                                                /note= "Wild-type Asp substituted
                                                             B or D protein useful for producing and additions to modified starch and ses mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.4%;
                                                                                                                                                                                                                                                                                                                                                                                        GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1475
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
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                                                                           a glucan useful
latexes in pape
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The invention an isolated protein comprising a glucosyltransferase B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D571K, D567T/D571K, D567T/D57TK, D567TK, D567TK,

Claim

36 •

Page; 44pp;

English

comprises mutations

paper

(GTF)

GTF D polypeptide having changes at positions from T589D, T589E, N N471D/T589D, and N471D/T589E. Also included are a glucan produced GTF mutant, an isolated polynucleotide which encodes Pl or P2, or I448V/D457N/D567T/D571K/K779Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589B, N471D,

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CC complementary polynucleotide, a ribonucleic acid sequence encoding the CC (STF mutant, an expression cassette comprising the polynucleotide operably CC (Inked to a promoter, a vector comprising the expression cassette, host CC cell introduced with the vector, a transgenic plant comprising the CC cell introduced with the vector, a glucan produced in a plant transformed CC with a gene encoding the mutant CTF, wild type or, starch, a latex, CC thermoplastic molecule or their combinations or glucan and starch where the glucan is produced in the amyloplast and/or vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a CC glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC conditions the glucan in a plant. The method comprises transforming a CC conditions to produce a regenerated plant cell under plant growing CC conditions to produce a regenerated plant and inducing expression of the CC regenerated plant, where the vector contains a transit sequence from CC ribulose biphosphate carboxylase small subunit, waxy, brittle-1 and glucan in the method or the vacuole of midar heef carboxylase small subunit, waxy, brittle-1 and glucan in the carboxylase small subunit, waxy, brittle-1 and glucan in the method comprise contains a transit sequence from contains a transit sequence from contains a transit sequence from the produced to the contains a transit sequence from the carboxylase small subunit, waxy, brittle-1 and glucan in the carboxylase small subunit, waxy, brittle-1 and glucan in the carboxylase from the vacuole of midar heef.
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닭
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. Glucans are useful as substitutes for and additions to modified starch and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic environmentally friendly.
                                                                                                                                                                                                                                                                                                                    Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          properties and impart gloss to the paper during coating step. The present sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU98036 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                 S. mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2002
                                                                                                                                                                                                                                                                     Streptococcus mutans
                                                                                                                                                                                                                                                                                                                  amyloplast;
                                                                                                                        Misc-difference
                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 VPSYSFIRAHDSEVQTLIADII 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VPSYSFARAHDSEVQDLIRDII 22
                                                                                                                                                                                                                                                                                                                                                                                                            glucosyltransferase GTFB mutant D567T/D571K
                                                                                                                                                                                                                                                                                                               vacuole; paper manufacture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                     Location/Qualifiers 567
                                                                                                 /note= "Wild-type Asp substituted by Lys"
                                                                                                                                          /note= "Wild-type Asp substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 1475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%;
86.4%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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1 VPSYSFARAHDSEVODLIRDII 22

Query Match Best Local

Similarity

77.3%; 81.8%;

Score 85; Pred. No. Mismatches

DB 5;

Length 1475

0

Gaps

0

Conservative

0;

Sequence 1475

A

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The invention an isolated protein comprising a glucosyltransferase (GTF) CC B polypeptide having changes at position from 1448V, D457N, D567T, D457N/D571K, D567T/D571K/K1014T, CC I1448V/D457N/D567T, D457N/D571K, D567T/D571K/K1014T, CC I448V/D457N/D567T,D571K/K70J4T, X169A/X170A/X17JA, and K779Q or a CC GTF D polypeptide having changes at positions from T589D, T589E, N471D, CC GTF D polypeptide having changes at positions from T589D, T589E, N471D, CC GTF mutant, an isolated polymucleotide which encodes Pl or P2, or its complementary polymucleotide, a ribonucleic acid sequence encoding the CC GTF mutant, an expression cassette comprising the polymucleotide operably clinked to a promoter, a vector comprising the polymucleotide operably collined to a promoter, a vector operation of plant comprising the vector, a transgenic plant comprising the coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, the glucan is produced in the amyloplast and/or vacuole or a maize line comprising the glucan in sproduced in the amyloplast and/or vacuole or a maize line comprising the glucan in a plant. The method comprises transforming a glucosyltransferase B or D enzyme, wild-type or mutant and a paper comprising the glucan in a plant. The method comprises transforming a plant cell with the vector, growing the plant cell under plant growing conditions to produce a time sufficient to produce the glucan in the conditions biphosphate carboxylase small subunit, waxy, brittle-1 and cclothologyllase biphosphate carboxylase small subunit, waxy, brittle-1 and glucan conditions composition of the polymologyllase mail subunit, waxy, brittle-1 and glucan conditions of the polymologyllase small subunit, waxy, brittle-1 and glucan conditions of the c
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07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
11-DEC-1998;
                                                chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. Glucans are useful as substitutes for and additions to modified starch and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in claim 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in papemanufacture, comprises mutations in specific positions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-414332/44
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95US-00485243.
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98US-00210361
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RESULT 19
AAU98037
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The invention an isolated protein comprising a glucosyltransferase (GTF) CC B polypeptide having changes at position from I448V, D457N, D567T, D457N/D57TK, D567T, D57TK/K1014T, CC I448V/D457N/D567T, D457N/D57TK, D567T/D57TK/K1014T, CC I448V/D457N/D567T/D57TK/K79Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a CC GTF D polypeptide having changes at positions from T589D, T589E, N471D, CC GTF mutant, an isolated polymucleotide which encodes P1 or P2, or its complementary polymucleotide, a ribonucleic acid sequence encoding the CC GTF mutant, an expression cassette comprising the polymucleotide operably clinked to a promoter, a vector comprising the expression cassette, host cell introduced with the vector, a transgenic plant comprising the coating composition comprising a glucan produced in a plant transformed coating composition comprising a glucan produced in a plant transformed coating gene encoding the mutant GTF, wild type or, starch, a latex, the glucan is produced in the amyloplast and/or vacuole or a maize line comprising the glucan is produced in the amyloplast and/or vacuole or a maize line comprising the glucan in a plant. The method comprises transforming a plant cell with the vector, growing the plant cell under plant growing conditions to produce a regenerated plant and inducing expression of the
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16-JAN-1998;
20-JAN-1998;
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07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                            36; Page; 44pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by Lys"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC polynucleotide for a time sufficient to produce the glucan in the CC regenerated plant, where the vector contains a transit sequence from CC ribulose biphosphate carboxylase small subunit, waxy, brittle-1 and CC chlorophyll AB binding protein to produce a transgenic plant, and glucan CC is produced in the amyloplast of potato or the vacuole of sugar beet. CC Glucans are useful as substitutes for and additions to modified starch CC and latexes in paper manufacture. Unlike prior aft techniques, which CC require input materials that produce chemical effluente, paper CC manufacture utilising the glucan produced by GTF, which utilises CC biologically produced input materials, is more cost-effective and CC environmentally friendly. Moreover, glucans also exhibit thermoplastic CC environmentally friendly to the paper during coating step. The present CC sequence represents a GTFB mutant of the invention. Note: The present CC using the GTFB sequence appearing as AAU98027 and the information in
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Query Match
Best Local &
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                                07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        S. mutans GTFB mutant I448V/D457N/D567T/D571K/K779Q/K1014T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU98038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Glucosyltransferase; coating composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU98038 standard; protein;
                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                            amyloplast; vacuole;
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                                                                                                         19-DEC-2000;
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11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 VPSYSFIRAHDSEVOTLIAKII 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                           2000US-00740274
           98US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
                                                          95US-00478704.
95US-00482711.
95US-00485243.
                                                                                                                                                                                                                                              /note= "Wild-type Asp
571
                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                              1014
                                                                                                                                                                                                                        /note=
779
                                                                                                                                                                                                                                                                                                457
                                                                                                                                                                                                                                                                                                                      448
                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                    /note= "Wild-type Lys
                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.3%;
                                                                                                                                                                                                                                                                                                                                                                                                       GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic
                                                                                                                                                                                                                                                                                                                                                                                            paper
                                                                                                                                                                                                                                                                                                           "Wild-type Ile substituted by Val"
                                                                                                                                                                                                           "Wild-type Lys
                                                                                                                                                                                                                                                                                  "Wild-type Asp
                                                                                                                                                                                                                                    "Wild-type Asp
                                                                                                                                                                                                                                                                                                                                                                                              manufacture; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1475
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.;
                                                                                                                                                                                     substituted by Thr'
                                                                                                                                                                                                             substituted
                                                                                                                                                                                                                                     substituted
                                                                                                                                                                                                                                                            substituted
                                                                                                                                                                                                                                                                                     substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1475;
                                                                                                                                                                                                                                     γď
                                                                                                                                                                                                              Λq
                                                                                                                                                                                                                                                            γď
                                                                                                                                                                                                                                                                                     γď
                                                                                                                                                                                                                                                                                      Asn"
                                                                                                                                                                                                                                                               Thr"
                                                                                                                                                                                                               Gln"
                                                                                                                                                                                                                                     Тув"
                                                                                                                                                                                                                                                                                                                                                                                                              molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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SAXARAXE
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                                                                                                                                                                                  ABR63235
                                                                                                                                                                                                   RESULT 21
                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC complementary polynucleotide, a ribonucleic acid sequence encoding the CC innked to a promoter, a vector comprising the polynucleotide operably CC linked to a promoter, a vector comprising the polynucleotide operably CC call introduced with the vector, a transgenic plant comprising the CC vector, a seed or tuber from the transgenic plant, a paper sizing and/or CC coating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTF, wild type or, starch, a latex, CC the glucan is produced in the amyloplast and/or vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a CC comprising the glucan in a plant. The wector vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a glucan in a plant. The method comprises transforming a plant growing the plant cell under plant growing CC comprising a glucan in a plant. The method comprises transforming a plant cell with the vector, growing the plant cell under plant growing CC riburles to produce a regenerated plant and inducing expression of the CC regenerated plant, where the vector contains a transit sequence from CC riburles binhosphate carboxylase small subunit, waxy, brittle-1 and CC riburles are useful as substitutes for and additions to modified starch CC and latexes in paper manufacture. Unlike prior art techniques, which cc require input materials that produce chemical effluents, paper CC manufacture utilising the glucan produced by GTF, which utilises CC plant growing the glucan in the specification but was created by the indexer custing step. The present CC using the GTFB sequence appearing as AAU98027 and the information in
                                                                                                                                                                                                                                                                                                                                             Matches
                 Glucansucrase sequence from strain
                                                         23-0CT-2003
27-AUG-2003
                                                                                                                       ABR63235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention an isolated protein comprising a glucosyltransierase (GIF) B polypeptide having changes at position from 1448V, D457N, D567T, K1014T, D457N/D571K, D567T, D457N/D571K, D567T/D571K, D567T/D571K/K1014T, L149A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D, M471D/T589D, and M471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polymelotide which encodes P1 or P2, or its GTF mutant, an isolated polymelotide which encodes P1 or P2, or its
                                                                                                                                                             ABR63235 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in page manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1475 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 36; Page; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-414332/44.
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                                                                                                                                                                                                                                                                 552
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                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                     VPSYSFARAHDSEVQDLIRDII 22
                                                                                                                                                                                                                                                               VPSYSFIRAHDSEVQTLIAKII 573
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                         (revised)
(first en
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                                                                                                                                                           protein; 2055 AA
                                                         entry)
                                                                                                                                                                                                                                                                                                                                                              77.3%;
81.8%;
                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                              Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                Mismatches
                     KG15
                                                                                                                                                                                                                                                                                                                                                                   DB 5;
3e-05;
                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                             Gape
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RESULT 22
ABR63236
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                    Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a sequence of the glucansucrase gene. (Updated on 23-OCT-2003 to standardise OS field)
20-JUL-2001; 2001EP-00202752.
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                           Glucansucrase sequence from strain Lb33.
                                                                                                                                                                                                                                                                                                  27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                      ABR63236 standard; protein; 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener.
                                                    22-JUL-2002; 2002WO-NL000495
                                                                                         30-JAN-2003
                                                                                                                              WO2003008618-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ACC84451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-289780/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-2001; 2001EP-00202752.
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
                                                                                                                                                                 Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Geel- Schutten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    955 IPNYSFVRAHDSEVQTVIGDIV 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPSYSFARAHDSEVQDLIRDII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.4%; ilarity 68.2%; Conservative
                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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6.5e-05;
3;
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TANA A RANG A RA

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RESULT 23
ABR63228
ID ABR63228
XX ABR63228
XX Gluca
XX Gluca
XX Gluca
XX Gluca
XX Gluca
XX Leucc
XX Leucc
XX Leucc
XX I Novel
DR N-PSI
XX Novel
PT Lain
XX Clain
XX Clain
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a sequence of the
                                                           Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3) - and alpha (1,6)-linked anhydroglucose units, useful as thickener.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van
                                 Claim 11; Page 27;
                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                        22-JUL-2002;
                                                                                                                                                                                                                                                                                                                        30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                  Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucansucrase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR63228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucansucrase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ACC84452
                                                                                                                                                                                                                                          20-JUL-2001; 2001EP-00202752.
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                                                                                                                      WO2003008618-A2
                                                                                                                                                                                                                                                                                                                                                                                     Leuconostoc
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                                                                                                                                                                                                            (NEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geel- Schutten
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                                                                                                                                             2003-289780/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucan produced by glucosyltransferase activity of lactic acid rium on sucrose substrate, and having backbone consisting of alpha
                                                                                                                                                                                                            ) NEDERLANDSE ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSYSFARAHDSEVQDLIRDII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSYSFVRAHDSEVOTVIAEIV 237
                                                                                                                                                                           Schutten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha (1,6)-linked
                                                                                                                                                                                                                                                                                                                                                                                    ф
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                                                                                                                                                                                                                                                                                        2002WO-NL000495
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                               51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .48;
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                                                                                                                                                                                                            TOEGEPAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain Lb86.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anhydroglucose units, useful as thickener.
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present invention relates to glucan capable of being produced

λq

Query Match Best Local S Matches 15

Similarity

71.8%; 71.4%;

15;

Conservative

w '-

Score 79; DB Pred. No. 0.00 3; Mismatches

; DB 7; 0.00033;

Length 1499;

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Gaps

0

Sequence 1499 AA;

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RESULT 24
ADC54806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                           (for example dextran) which uses D-glucoses, such as a starch and a cellulose, as a structural unit. The modified enzyme of the invention is useful in the manufacture of glucan. The selection of the active centre area of DS which carries out transduction, enables changes in structure and character of an enzyme-reaction product and their application to various uses. The present sequence is that of a protein which is related to the Leuconostoc mesenteroides dextran sucrase protein and which was used during the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the
                                                                                                                                                                                                                           Example 1; SEQ ID NO 11;
                                                                                                                                                                                                                                                      Novel modified dextran sucrase which exchanges one site of active center zone of dextran sucrase for active center zone of different types of dextran sucrase, useful for manufacturing glucan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dextran sucrase; active centre D-glucose; starch; cellulose; enzyme-reaction product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC54806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal tract. The present sequence represents a sequence of the
                                                                                                                                                                                            Thie
                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                         WPI; 2003-735670/70.
                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2001; 2001JP-00307067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC54806 standard; protein; 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glucansucrase gene
                                                                                                                                                         This invention relates to a modified dextran sucrase (DS) exchanging or site of the active centre zone of a dextran sucrase for the active cent zone of different types of dextran sucrase. Glucan is a polysaccharide
                                                                                                                                                                                                                                                                                                                                                                        (DOKU-) DOKURITSU GYOSEI HOJIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq ID11 related to L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                        ADC54814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPNYSEVRAHDSEVOTVIAQII 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       active centre zone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.7%;
                                                                                                                                                                                                                           28pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 80; DB
Pred. No. 2.3e
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucan
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                                                                                                                                                                                                                                                                                                                                                                        SHOKUHIN SOGO KEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucan; poly:
manufacture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polysaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transduction;
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                                                                                                                                                                                              (DS) exchanging one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dextran;
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AAU80055
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                                                              Query Match
Best Local S
Matches 14
                                                                                                                                                         is used to produce yoghurt, curd, cheese or other fermented milk products, ice cream, fermented cereal products, water-based jellies, infant formulae and pet foods. Dextransucrase can also be bound to e.g. vitamins or oral vaccines for delivering these to foods, using (A) as carrier. The method produces foods with attractive and uniform texture, since dextransucrase is evenly distributed and forms a thickening agent in situ, with the amount formed being controlled by the amount of dextransucrase bound. Milk does not have to be coagulated in order to achieve a good texture, so the amount of acidic by-products formed is reduced. Dextransucrase binds to many different types of cells over wide ranges of temperature and pH and the treated bacteria can be stored in liquid or powdered form. The present sequence represents the amino acid sequence of dextransucrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dextransucrase; yoghurt; curd; cheese; fermented milk; infant formulae; pet food; vitamin; oral vaccine; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-2002
                                                                                                                               Sequence 1527 AA;
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to preparation of a fermented food product that includes treating the microorganism (A) to be used for fermentation with a dextransucrase so that this binds to the cell walls of (A). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1201131-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leuconostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leuconostoc mesenteroides dextransucrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU80055
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 14-20; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparing fermented food products, e.g. yoghurt, using microorganisms that have dextran sucrase bound to the surface, provide attractive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABK50932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2000; 2000EP-00123012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU80055 standard; protein; 1527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uniform texture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bauche A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2000; 2000EP-00123012
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 652
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                                1 VPSYSFARAHDSEVQDLIRDII 22
                                                                                Similarity
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:|:||| ||||||| :| |:
IPNYSFVRAHDSEVQTVIAQIV 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNYSFVRAHDSEVQTVIAEII 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Maleprade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mesenteroides.
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                              71.8%;
63.6%;
                                                              4
                                                              Score 79; DB Pred. No. 0.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neubauer H,
                                                                                0.00033;
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                                                                                             Length 1527;
                                                                  Indels
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                                                              Gaps
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RESULT 26
ADC54807
ID ADC54

ADC54807 standard; protein; 1527 AA

18-SEP-2003

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RESULT 27
ADD93658
ID ADD93
X S X F X G X S X S X G X G X
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a modified dextran sucrase (DS) exchanging one site of the active centre zone of a dextran sucrase for the active centre zone of different types of dextran sucrase. Glucan is a polysaccharide (for example dextran) which uses D-glucoses, such as a starch and a cellulose, as a structural unit. The modified enzyme of the invention is useful in the manufacture of glucan. The selection of the active centre area of DS which carries out transduction, neables changes in structure and character of an enzyme-reaction product and their application to various uses. The present sequence is that of the Leuconostoc mesenteroides dextran sucrase protein used during the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1527 AA;
                                                                                               Glucosyltransferase; enzyme; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel modified dextran sucrase which exchanges one site of active zone of dextran sucrase for active center zone of different types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADC54802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2001; 2001JP-00307067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme-reaction product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dextran sucrase; active centre zone; glucan; polysaccharide; de D-glucose; starch; cellulose; glucan manufacture; transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003
                                                                   Streptococcus sobrinus
                                                                                                                         Streptococcus sobrinus glucosyltransferase-U
                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                     ADD93658;
                                                                                                                                                                                                                 ADD93658 standard; protein; 1554 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 12; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dextran sucrase, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-735670/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leuconostoc mesenteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leuconostoc mesenteroides dextran sucrase protein.
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                                       WO2003075845-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOKU-) DOKURITSU GYOSEI HOJIN SHOKUHIN SOGO KEN
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                   1 VPSYSFARAHDSEVQDLIRDII 22
                                                                                                                                                                                                                                                                                         IPNYSFVRAHDSEVQTVIAQIV 673
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                              71.8%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for manufacturing glucan.
                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               DB 7;
                                                                                                                                                                                                                                                                                                                                                                 .00033;
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                                                                                                                                                                                                                                                                                                                                                                             Length 1527;
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RESULT 28
ABR63229
ID ABR63229
XX ABR63229
XX ABR63229
AC ABR63
XX ABR63
XX Gluca
XX Gluca
XX Gluca
XX Holoac
XX Leucc
XX MO200
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XX Van (NEDB
XX WPI;
DR WPI;
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II protein-binding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multispitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2002;
08-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosyltransferase-U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-845091/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
Novel glucan produced by glucosyltransferase
                                                                       Van Geel- Schutten
                                                                                                                                                                                                                                                                                                Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
                                                                                                                                                                                                                                                                                                                                            Glucansucrase
                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                       ABR63229;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR63229 standard;
                                                                                                                                   20-JUL-2001;
25-JUL-2001;
                                                                                                                                                                             22-JUL-2002; 2002WO-NL000495
                                                                                                                                                                                                          30-JAN-2003
                                                                                                                                                                                                                                       WO2003008618-A2
                                                                                                                                                                                                                                                                    Leuconostoc sp
                                                                                                       (NEDE ) NEDERLANDSE ORG TOEGEPAST
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                             2003-289780/28.
)B; ACCS0073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taubman
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2002US-0402483P.
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2001EP-00202841
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                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                         H
                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s the protein sequence of Streptococcus sobrinus (GTF-U). Peptide fragments of GTF-U, especially
                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                     221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                                                                                              strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dental caries comprises a fragment of
to a major histocompatibility complex
                                                                                                                                                                                                                                                                                                                                              TP86
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   activity
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    lactic
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ABB98651
ID ABB
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSR-E; glycosyl transferase; dextran; prebiotic; microflora regulation; intestinal transit; minera colon cancer; acne; dandruff; body odour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterium on sucrose substrate, and having backbone consisting \{1,3\} - and alpha \{1,6\} -linked anhydroglucose units, useful as t
The present invention relates to a novel dextran saccharase, DSR-E (ABB99574), from Leuconostoc mesenteroides MRRL B-1299. The saccharase has glycosyl transferase activity suitable for producing dextrans having alpha(1-2) branches from sucrose, p-nitrophenyl-alpha-D-glucopyranoside, alpha-fluoroglucose, alpha-D-glucopyranoside or alpha-D-galactopyranosyl-sucrose. The dextran saccharase is useful in prebiotic, pharmaceutical or cosmetic compositions. The dextrans and related compounds having alpha(1-2) bonds, produced using DSR-E, may be
                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-2003
14-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB98651 standard; peptide;
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                                                                                                                                                                New glycosyl transferase enzymes, domains and producing alpha-(1-2) pharmaceutical or cosmetic composi
                                                                                                                                                                                                                                                        Bozonnet
                                                                                                                                                                                                                                                                                                                                            19-DEC-2001;
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                                                                                                                                      Example 2; Fig 5; 82pp; French
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Pred. No. 7.6e
4; Mismatches
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7.6e-05;
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RESULT 30
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  Matches
                                                                                                                                                                             The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involved in signalling/cellular recognition processes in vivo (specifically in regulation of microflora in the intestines or on the skin); and are potentially useful for improving intestinal transit, increasing assimilation of minerals (e.g. calcium and/or magnesium), preventing cancer of the colon and combating skin problems such as acne, dandruff and body odour. The present sequence is a conserved peptide sequence from the catalytic domain of the DSR-E of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
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25-JUL-2001; 2001EP-00202841.
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                                                                                                       Sequence 221 AA;
                                                                                                                                                            glucansucrase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 24-25; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACC50070.
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Search completed: May 4, 2004, 09:10:01 Job time : 50.6667 secs

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AF1966
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AF19691
AF196

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J. Bacteriol. 173, 989-996, 1991
A,Title: Peptide sequences for sucrose splitting and glucan binding within Streptococcus A,Reference number: A38175; MUID:91123227; PMID:1704006
A,Accession: A38175
A;Description: catalyzes the synthesis of both water-soluble and water-insoluble C;Superfamily: cpl repeat homology C;Keywords: duplication; glycosyltransferase; hexosyltransferase F;1-34/Domain: esjual sequence #status predicted <SIG> F;35-1375/Pyroduct: glucosyrransferase #status predicted <WAT> F;1126-1145/Domain: cpl repeat homology <CP1> F;1138-1337/Domain: cpl repeat homology <CP2> F;1318-1337/Domain: cpl repeat homology <CP2>
                                                                                                                                                                                                                                                                                            A,Experimental Bource: GS-5
R,Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4270, 1987
A,Title: Sequence analysis of the 9tfB gene from Streptococcus mutans.
A,Reference number: A33135; MUID:87308013; PMID:3040685
A,Accession: C33135
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A; Residues: 1-1592 < ABO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Sequence analysis of the gtfC gene A;Reference number: JT0345; MUID:89137980; FA;Accession: JT0345
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                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-349 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1375 < UED >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: JT0345; C33135
R;Ueda, S.; Shiroza, T.; Kuramitsu, H.K.
                                                                                                                                                                                                                 A;Cross-references: GB:M17361
                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pecies: Streptococcus mutans;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992
                                                                                                                                                              Function:
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Pred. No. 1
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pmID:2976010
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R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4270, Bacteriol. 169, 263-4270, Battle: Sequence analysis of the 9tfB gene from Streptococcus mutans.
A;Reference number: A33135; MUID:87308013; PMID:3040685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtfB protein precursor - Streptococcus mutans C;Speciles: Streptococcus mutans C;Speciles: Streptococcus mutans C;Date: 23-Oct-1990 #sequence revision 23-Oct-1990 C;Accession: B33135; A33128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-171,173-641,'N',643-1475 <SH2>
A;Experimental source: strain GS-5
C;Superfamily: cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A33128
A; Accession: A33128
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                                                                                                                                                                                                                                                                                            C;Accession: JC5473
R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, P. Gene 182, 23-32, 1996
A;Title: Cloning and sequencing of a gene coding for a novel dextransucrase A;Reference number: JC5473; MUID:97136686; PMID:8982063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1475 <SHI>
                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1290 <MON>
A;Cross-references: GB:U38181
C;Comment: This enzyme catalyzes the transfer
                                                                                                                                                                                                                                                                                                                                                                                                             dextransucrase (BC 2.4.1.5) - Leuconostoc mesenteroides
C;Species: Leuconostoc mesenteroides
C;Date: 07-Jul_1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
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Best Local S
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                                                                  922-1290/Domain:
                                                                                    Keywords: glycosyltransferase; hexosyltransferase; 78-870/Domain: catalytic #status predicted <CAT>
Query Match
Best Local
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                                                             glucan-binding #status predicted
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75.5%;
76.2%;
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Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99; DB 2;
Pred. No. 3.6e-07;
0; Mismatches 2
    Score 83; DB 2;
Pred. No. 0.00011;
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16;

Conservative

Mismatches

Indels

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Gaps

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Similarity

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RESULT 7
S22737
                                  glucosyltransferase (EC 2.4.1.-) S - Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_chance_recession: S22737; S28810; B44811; S22727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infect. Immun. 58, 2452-2458, 1990
A; Title: Analysis of the Streptococcus downei gtfS gene,
A; Reference number: A41483; MUID: 90316665; PMID: 2142479
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FEMS Microbiol. Lett. 159, 307-315, 1998
A;Title: Cloning and sequencing of a gene coding for an extracellular dextransucrase (DSA;Reference number: Z20981; MUID:98164374; PMID:9503626
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C;Species: Leuconostoc mesenteroides
C;Date: 22-Oct.1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
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C;Keywords: glycosyltransferase; hexosyltransferase
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A;Residues: 1-1365 <GIL>
A;Cross-references: GB:M30943; NID:g153652; PIDN:AAA26898.1; PID:g153653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptococcus sobrinus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999
C;Accession: A41483
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A;Experimental source: strain NRRL B-1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A41483; A; Accession: A41483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucosyltransferase (EC 2.4.1.-) gtfS precursor - Streptococcus sobrinus
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  submitted
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to the EMBL
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Data Library, March 1992
                                                                                                                                                                                                                                                                                                      63.6%;
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68.2%;
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Pred. No.
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Pred. No.
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RESULT 8
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A;Cross-references: EMBLEZ11872; NID:g47530; PIDN:CAA77898.1; PID:g47531

A;Experimental source: ATCC 25975

R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A.

J. Gen. Microbiol. 137, 2577-2593, 1991

A;Title: Molecular characterization of a cluster of at least two glucosy

A;Reference number: A44811; MUID:92148377; PMID:1838391

A;Accession: S28810
                                                                                                                                                                                                                                                                               RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: gtfK
C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyl
F;1456-1475/Domain: cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1449 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 63, 609-621, 1995
A;Title: Streptococcus salivarius ATCC 25975 possesses at least A;Reference number: 220909; MUID:95122197; PMID:7822030
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C;Genetics:
                                                                                                                              R)Jaffe, R.I. submitted to the EMBL Data Library, February 1998 a. nearription: Streptococcus salivarius V1477 gtf
                                                                                                                                                                                             glucosyltransferase N - Streptococcus salivarius (fragment) C;Species: Streptococcus salivarius C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_ch_C;Accession: T30552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:L35495; NID:g662378; PID:g662379; PIDN:AAC41412.1
C;Genetics:
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A; Molecule type:
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A;Cross-references: EMBL:AF049609; NID:g2935545; PID:g2935546; PIDN:AAC05156.1
C;Genetics:
                                                    A;Status: preliminary; translated A;Molecule type: DNA
                                                                                              A; Reference number: Z20854
A; Accession: T30552
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A;Residues: 1-51 <GIF>
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Pred. No. 0.016;
2; Mismatches
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Pred. No. 0.03;
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C; Species.
C; Atc: 30. Sep-1993 ....
C; Accession: A45866
C; Accession: A45866
R; Honda, O; Kato, C; Kuramitsu, H.K.
R; Honda, O; Kato, C; Kuramitsu, H.K.
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C;Species: Streptococcus salivarius
C;Species: Streptococcus salivarius
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 15-Oct-1999
C;Accession: A44811; S22726; $\overline{S}28809$
C;Accession: A44811; S22726; $\overline{S}28809$
C;Accession: A,04811; S227253, 1991
J. Gen. Microbiol. 137, 2577-2593, 1991
J. Gen. Microbiol. 137, 2577-2593, 1991
A;Title: Molecular characterization of a cluster of at least two glucosyltransferase gen
A;Reference number: A44811; MUID:92148377; PMID:1838391
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A;Reference number: A45866; MUID:91100958; PMID:2148600
A;Accession: A45866
A;Status: preliminary
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A;Residues: 1-1518.<GIF>
A;Residues: 1-1518.<GIF>
A;Cross-references: EMBL.Z11873; NID:947526; PIDN:CAA77900.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:81050, NCA)
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F;1192-1211/Domain: cpl repeat homology <CP3>
F;1192-1211/Domain: cpl repeat homology <CP4>
F;1257-1276/Domain: cpl repeat homology <CP5>
F;1277-1297/Domain: cpl repeat homology <CP5>
F;1321-1340/Domain: cpl repeat homology <CP6>
F;1341-1361/Domain: cpl repeat homology <CP6>
F;1341-1361/Domain: cpl repeat homology <CP6>
F;1365-1404/Domain: cpl repeat homology <CP7>
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C;Superfamily: cpl repeat homoloc
C;Keywords: glycosyltransferase;
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A; Residues: 1-1431 < HON>
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13; Conserv
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          NYIFIRAHDSEVQTVIAKII 595
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Pred. No. 0.094;
                                                                                                                                                                         Score 62; DB 2;
Pred. No. 0.26;
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NCBIP:81052)
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                     A;Status: preliminary
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glucosyltransferase - Streptococcus salivarius C,Species: Streptococcus salivarius C,Species: Streptococcus salivarius C,Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 C,Accession: T30856
R,Simpson, C.L.; Giffard, P.M.; Jacques, N.A.
hypothetical protein VCA0471 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C.Species: Vibrio cholerae C.Boecies: Vibrio cholerae C.Boecies: Vibrio cholerae C.Boecies: Vibrio cholerae C.Boecies: Vibrio cholerae C.Boecession: G82455 C.Boecession: G82455 C.Boecession: G82455 C.Boecession: G82455 C.Boecession: Galaxies C.Boecession: Galaxies C.Boecession: Galaxies C.Boecession: C.Boecession: D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, C.Boecession: G82455 C.Boecession: G82455 C.Boecession: G82455 MUID:20406833; PMID:10952301 A, Accession: G82455 MUID:20406833; PMID:10952301 A, Accession: G82455 C. Control of Colerae C.Boecession: G82455 C. Control of Colerae C.Boe
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C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-1577 <SIM>
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A;Title: Sequence analysis of the genome of the unicellular cyanobacter
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C;Species: Symechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr_1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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A;Status: preliminary
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A; Residues: 1-108 < KAN>
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Pred. No. 1.5;
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Pred. No.
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Yamada, M.; Ya
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A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440;
A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440;
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83788
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 27-Oct-2003
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A;Cross-references: GB:AE004379; GB:AE003853; NID:g9657865; PIDN:AAF96375.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A;Experimental source: serovar 3; biovar 1
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A; Residues: 1-597 < GLA>
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                                                                                                                                                                                                                                                                                                                                                                          C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82935
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A;Map position: 2
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                                                                                                                                            A;Genetic code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.7%;
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; Pred. No. 19;
2; Mismatches
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                                                                                     Score 47;
Pred. No.
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19;
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                                                                                                      Length 597
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                                                                     Indels
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                                                    RESULT 19
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N;Alternate
C;Species: D
                retrovirus-related
N;Alternate names:
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1229
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-603 cGLA>
A;Cross-references: GB:NC 003210; PIDN:CAC9312.1; PID:g16410650; GSPDB
A;Experimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                  D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              excinuclease ABC chain C homolog uvrC [imported] - Listeria innocua (strain Clig C;Species: Listeria innocua C;Spate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AD1582 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, L.; Dussurget, O.; Entian, K.D.; F.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: uvrC C; Superfamily: excinuclease ABC chain C
                                                                                                                                                                                                                            A;Cross-references: GB:AL592022; PIDN:CAC96428.1; A;Experimental source: strain Clip11262 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision
                                                                                                                                                                                   A;Gene: uvrC
C;Superfamily: excinuclease ABC chain
                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-603 <GLA>
                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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                                             1 VPSYSFARAHDSEVQDLIRDII 22
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VRSY-FSGTHDSKTORLVQEIV
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                                                                                             Conservative
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Pred. No. 28;
6; Mismatches
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Pred. No. 28;
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cian, K.D.;
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Voss, H.; Wehland,
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Voss, H.; W
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Fmihi, H.
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Wehland,
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H

-related pol polyprotein - fruit
e names: reverse transcriptase
Drosophila melanogaster

fly (Drosophila melanogaster) retrotransposon

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A;Title: Identification of the coding sequence for a reverse transcriptase-like A;Reference number: A93349; MUID:85061628; PMID:6209583
A;Accession: A03971
A;Molecule type: DNA
A;Residues: 1-1058 <SAI>A;Residues: 1-1058 <SAI>A;Cross-references: GB:X01472; GB:J01060; GB:J01061; NID:g8142; PIDN:CAA25702.1; C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: FlyBase:FBgn0000004
C;Superfamily: pol polyprotein
C;Keywords: polyprotein; reverse transc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atrazine chlorohydrolase homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence
C;Accession: T47184
                                                                A; Experimental source: adult C; Genetics:
                                                                                                                                                                                                 submitted to the Protein Sequence Database, March A;Reference number: Z24375 A;Accession: T47184
                                                                                                                                                                                                                                                                                                                                hypothetical protein DKFZp434F1526.1 - human (fragment)
C;Species: Homo Bapiens (man)
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                                              A;Note:
                                                                                                          A; Cross-references: EMBL: AL162051
                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-506 < AAA>
                                                                                                                                                                                                                                                                    R; Ansorge, W.; Wirkner, U.; Mewes, H.W.; Weil,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1~330 <KLE>
                                                                                                                                                                        A;Status: preliminary
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Best Local S
Matches 7
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Best Local
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                                              DKFZp434F1526.1
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42.1%;
    40.0%;
                                                                                          testis; clone
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Pred. No. 35;
6; Mismatches
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Pred. No.
      Score 44;
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                                                                                            DKFZp434F1526
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      DB
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      Length 506;
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hypothetical protein F53B3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                      RESULT
                                                                            C;Accession:
                                                                                                                                                                 T16450
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Query

Match

November 1995 legans cosmid

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A, Map position: 5p14-5p13

A, Map position: 5p14-5p13

C, Superfamily: natriuretic peptide receptor C; natriuretic peptide-binding domain homolocy, cysuperfamily: natriuretic peptide receptor C; natriuretic peptide receptor; transmembrz C; Keywords: alternative splicing; glycoprotein; homodimer; hormone receptor; transmembrz F; 12-23/Domain: signal sequence #status predicted <SIG>
F; 24-45/Domain: propeptide #status experimental <PRO>
F; 24-45/Domain: propeptide #status predicted <EXT>
F; 46-479/Domain: extracellular #status predicted <EXT>
F; 131-462/Domain: natriuretic peptide-binding domain homology <NPB>
F; 483-503/Domain: transmembrane #status predicted <TMM>
F; 483-503/Domain: transmembrane #status predicted <TMM>
F; 66, 293/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 394/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F; 394/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-475,'SG',477-540 <POR>
A;Residues: 1-475,'SG',477-540; NID:gl78651; PIDN:AAA51734.1; PID:gl78652
A;Cross-references: GB:M59305; NID:gl78651; PIDN:AAA51734.1; PID:gl78652
A;Note: alternative splice form C5
R;Stulte, J.T.; O'Connell, K.L.; Garcia, C.; Wong, S.; Engel, A.M.; Garbers, D.L.
Blochemistry 33, 11372-11381, 1994
A;Title: The disulfide linkages and glycosylation sites of the human natriuretic
A;Reference number: A55870; MUID:95244450; PMID:7727388
A;Contents: annotation; propeptide, disulfide bonds, carbohydrate binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lowe, D.G.; Camerato, T.R.; Goeddel, D.V.
Nucleic Acids Res. 18, 3412, 1990
A;Title: cDNA sequence of the human atrial
A;Reference number: S10150; MUID:90287735;
A;Accession: S10150
A;Molecule type: mENA
A;Molecule type: mENA
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R; Porter, J.G.; Arfsten, A.; Fuller, F.; Miller, J.A.; Gregory, L.C.; Lewicki, J.A.
Biochem. Biophys. Res. Commun. 171, 796-803, 1990
B; Title: Isolation and functional expression of the human atrial natriuretic peptide
A; Title: Isolation and functional expression of the human atrial natriuretic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A35896; MUID:90386656; PMID:2169733
A;Accession: A35896
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N;Alternate names: atrial natriuretic facto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-540 <LOW>
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                                                                                                                                                      Query Match
Best Local 9
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234 YSFDETKOLDLEDIVÁNÍ
                                                                                                                            Similarity 7; Conserv
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Conservative
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                                                                                                                                                         40.0%;
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   251
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Pred. No. 62;
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factor clea
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PMID:2162522
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glutamy1-tRNA synthetase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89820
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology C;Keywords: carrier protein; phosphopantetheine; phosphoprotein F;505-946/Domain; acetate-CoA ligase homology <ACL1> F;964-1032/Domain; acyl carrier protein homology <ACL2> F;1942-1978/Domain; acetate-CoA ligase homology <ACL2> F;1942-1978/Domain; acetate-CoA ligase homology <ACCP2> F;1996-2063/Domain; acetate-CoA ligase homology <ACCP2> F;3046-3483/Domain; acetate-CoA ligase homology <ACCP2>
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A;Title: The bacitracin biosynthesis operon of Bacillus 1.
A;Reference number: Z21058; MUID:98089193; PMID:9427658
A;Accession: T31679
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C;Genetics:
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A; Accession: T16450
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F;4078-4526/Domain: acetate-CoA ligase homology <ACP4>
F;4542-4669/Domain: acyl carrier protein homology <ACP4>
F;5593-603/Domain: acetate-CoA ligase homology <ACP4>
F;5593-603/Domain: acetate-CoA ligase homology <ACP5>
F;6050-6118/Domain: acyl carrier protein homology <ACP5>
F;3532/Binding site: phosphopantetheine (Ser) (covalent)
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A; Residues: 1-6359 < KON>
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C;Species: Bacillus licheniformis
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Pred. No. 77;
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Pred. No. 1.1e+03
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A;Molecule type: DNA
A;Residues: 1-484 <KIN>
A;Cross-references: GB:BAD0001B; PID:g13700418; PIDN:BAB41716.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: gltX
C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein BH1358 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence revision 01-Dec-2000 #sequence revision 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83819
                                                                                                                                                                                                                                                                                             R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyri A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-176 <STO>
                                                                                                                                                                        A; Experimental source: C; Genetics:
                                                                                                                                                                                 A;Residues: I-195 <KAW>
A;Cross-references: DDBJ:AP000059; NID:g5103911; PIDN:BAA79242.1; PID:g5103926
A:Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C;Accession: F72718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05077.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                  A;Gene: APE0287
                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                           Superfamily: Aeropyrum pernix hypothetical protein APE0287
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9; Conserv
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VPSYSFARAHDSEVQDLIRDII 22
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Pred. No. 65;
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Pred. No.
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Pred. No. 24;
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I. Nucleic Acids Res. 29, 2145-2153, 2001
A;fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pull A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: H90599
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F70332
                                                                                                                      conserved hypothetical protein MYPU_7040 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: H90599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proline-tRNA synthetase - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999 C;Accession: F70332 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleolar protein NOP5-like protein [imported] - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T50180 C;Accession: T50180 R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                        RESULT 30
H90599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: F70332
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A; Introns: 6/1; 40/2
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A;Molecule type: DNA
A;Residues: 1-508 <BAD>
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A,Experimental source: strain VF5
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Pred. No.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-631 <KUR>
A;Residues: 1-631 <KUR>
A;Cross-references: GB:AL445566; PID:g14090119; PIDN:CAC13877.1; GSPDB:GN00153
A;Cross-timental source: strain UAB CTIP
C;Genetics:
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A;Genetic code: SO
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                                                                                                                                                                  C; Superfamily: conserved hypothetical protein MG139
Search completed: May 4, 2004, 09:13:19
Job time : 15.6667 secs
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version (c) 1993 - 2004
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GALT_BACHD
UVRC_LISIN
GCSP_XYLFT
FOL3_DROME
SYL STRAE
SYL ST
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Y326_MYCGE
PMRF_LYMST
MITF_MOUSE
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YP71 CAREL
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SYE MYCPN
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DEF2 ANASP
TOP1 SPVKA
MI2D BACSU
DP1 RAT
ARC2 RHIME
Y892 MYCTU
ANC BOVIN
PRIM BACSU
Y115 MYCLE
HTPG STRCO
Y893 HUMAN
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P11A_HOVAN
PRAX_HUMAN
CYCG_CYACA
DCD_CYACA
PIP NEIGO
PITZ_PYHO
MDHP_FABI
SYD_XANCA
SYD_XANCA
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SYD_XANCA
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3 rattus morv
5 rhizobium m
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9 mycobacteri
1 streptomyce
7 homo sapien
4 xylella fas
1 bos taurus
6 homo sapien
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01-JUL-1989
01-JUL-1989
10-OCT-2003
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-I- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUSEN OF THE DENTAL PLAQUE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE
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"Nucleotide sequence
sobrinus MFe28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-UUL-1989 (Rel. 11, Created)
01-UUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last amootation updat
Glucosyltransferase-I precursor (EC 2.4.1.5
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87308014; PubMed=3040686; Ferretti J.J., Gilpin M.L., Russell R.R.B.; "Nucleotide sequence of a glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=MFE28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus downei (Streptococcus sobrinus).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                         REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                            REPEAT
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REPEAT
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).

    -!- SIMILARITY: Belongs to family 70 of glycosyl hydro
    -!- SIMILARITY: Contains 19 cell wall binding repeats.

                                                                                                                                                                                                                                                                                                                                                              EMBL; M17391; AAC63063.1;
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                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                               RPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPI
1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: Sucrose + (1,6)-alpha-D-glucosyl)(N)

fructose + {(1,6)-alpha-D-glucosyl)(N+1).

SUBCELLULAR LOCATION: Secreted.
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554
                                                                                                                                                                                                                                                                                                          Pro; IPR00247; CW binding.
Pro; IPR003318; GW binding. 70.
PP001473; CW binding I; 16.
PP02324; Glyco_hydro_70; 1.
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                                                            Similarity
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VPSYSFARAHDSEVODLIRDII 575
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1099
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11227
1292
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1406
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llarity 100.0%;
Conservative
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CATALYTIC (APPROXIMATE
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                                                              Score 110; DB 1;
Pred. No. 2.1e-09;
                                                                                                                REPEAT
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                                                  Mismatches
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B,
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                                                                                                                                                                                                                                                            (APPROXIMATE).
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01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5) (GTF-I) (De (Sucrose 6-glucosyltransferase).
Streptococcus downel (Streptococcus sobrinus).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D90213; BAA14241.1; -
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro_70.
Pfam; PF01473; CW binding 1; 13.
Pfam; PP02324; Glyco hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetase).";
J. Bacteriol. 1
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MRDLINE=91123227; PubMed=1704006;
Abo H., Matsumura T., Kodama T.,
                                                                                                                                                                                                                            DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - |- CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Peptide sequences for sucrose splitting and glucan binding within Streptococcus sobrinus glucosyltransferase (water-insoluble glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Glycosyltransferase; Signal; Repeat;
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to f
SIMILARITY: Contains 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANBOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPH
1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES
FORMS OF GLUCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fructose + {(1,6)-alpha-D-glucosyl}(N+1).
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGH
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BEC
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                      Similarity 95.9
21; Conservative
                             VPSYSFARAHDSEVQDLIRDII
     VPSYSFARAHDSEVQDIIRDII
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CATALYTIC (APPROXIMATE)
GLUCÂN-BINDING (APPROXI
6.5 X TANDEM REPEATS.
                                                                                                                                                                                                            ₹
                                                                                                                              Score 108; DB 1;
Pred. No. 4.5e-09;
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                                                                                                                                                                                                         (INCOMPLETE).
BCOA66D079351ECF CRC64;
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                                                                                                        Mismatches
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RESULT 3
GTFB_STRMU
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P08987; O693
01-NOV-1988
           EMBL;
EMBL;
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Kimura S., Hamada S.;
"Molecular analyses of
Streptococcus mutans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=MT4239 / Serotype C, MT4245
MT4467 / Serotype E, and MT8148 / S
MEDLINE=98231643; PubMed=9570124;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87308013; PubMed=3040685; Shiroza T., Ueda S., Kuramiteu H.K.; Shiroza T. analysis of the gtfB gene: "Sequence analysis of the gtfB gene: J. Bacteriol. 169:4263-4270(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales;
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                                                                                                                                                                                                                                                                           C. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS.

TO PLAY A KEY ROLLE IN THE DEVELOPMENT OF THE DENTIAL PLAQUE BECAUSE

OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE

AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCTOSE + {(1,6)-alpha-D-glucosyl}(N) = D-fractose + {(1,6)-alpha-D-glucosyl}(N+1).

SUBCELLAULAR LOCATION: Secreted.

MISCELLAULAR LOCATION: Secreted.

MATER-SOLUBLE GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES BOTH

1,3-LINKED GLUCOSE AND SOME 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                    SIMILARITY: Belongs to family 70 of SIMILARITY: Contains 10 cell wall
          FORMS
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                                                                                                                                      and this statement is not requires a license agreeme
                                                                                                                                                                                                                                                                  OF GLUCANS.
                                                                                                                         equires a license agreement (S email to license@isb-sib.ch).
                      AAA88588.1; -... BAA26103.1; -... BAA26105.1; -... BAA26109.1; -... BAA26113.1; -... BAA26113.1; -... BAA26119.1; -...
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O69387; O69390; O69396;
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wall binding repeats.
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CM_binding I; 7.
Pfam; PF02324; Glyco_hydro_70; 1.
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ADS -> VDG
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GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE)
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NS GS-5, MT4245,
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                        Gaps
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RESULT 4
GTFC_STRMU STANDARD; PRT; 1455 AA.

ID GTFC_STRMU STANDARD; PRT; 1455 AA.

AC P13470; O69382; O69385; O69388; O69391; O69397; ID O1-NOV-1988 (Rel. 09, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucosyltransferase-SI precursor (EC 2.4.1.5) (GUBE (Dextransferase) (Sucrose 6-glucosyltransferase)
GN GTFC OR SMU.1005.
MEDIATINE-22395063; PubMed=12397186;
MEDIATINE-22395063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
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Shiroza T., Ueda S., Kuramitsu H.K.;
Shiroza T., Ueda S., Kuramitsu H.K.;
"Sequence analysis of the gtfB gene from Streptococcus mutans.";
J. Bacteriol. 169:4263-4270(1987).
-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAN
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
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STRAIN-MT4239 / Serotype C, MT4245
MT4467 / Serotype E, and MT8148 / SMT4467 / Serotype E, and MT8148 / SMT4467 / Serotype E, and MT8142 / MEDLINE-98231643; PubMed=9570124;
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                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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"Molecular analyses of glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiwara T., Terao Y., Hoshino
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                                                                                                                                                                                        FORMS OF GLUCANS.
SIMILARITY: Belongs to family 70
SIMILARITY: Contains 5 cell wall
                                                                                                                                                                                                                                           AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCYOSE + {(1,6)-alpha-D-glucosyl} (N)

fructose + {(1,6)-alpha-D-glucosyl} (N+1).a-

SUBCELLULAR LOCATION: Secreted.

NISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS

NISCELLANEOUS: GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS

1,3-LINKED GLUCOSE AND SOME 1,6-GLUCOSE). GTF-SI SYNTHESI
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 M22054; AAA88592.1;
D88652; BAA26102.1;
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JA159 / ATCC 700610 / Serotype
-22295063; PubMed=12397186;
-72295063; PubMed=12397186;
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EMBL; D88658; BAA26110.1; -.
EMBL; D88661; BAA26110.1; -.
EMBL; D89978; BAA26120.1; -.
EMBL; AE014940; AAN88706.1; -.
EMBL; M17361; AAA88589.1; -.
PIR; JT0345; JT0345.
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Pro; IPR00318; Glyco hydro 70.
PR01473; CW binding I, 8.
PR02324; Glyco hydro 70; 1.
Iferame; Glycosyltransferase; Si
  20;
                      Similarity
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CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
2.4 A, 1 C AND 1 AC REPEATS.
A REPEAT.
A REPEAT.
A REPEAT.
A REPEAT (INCOMPLETE).
V -> I (IN STRAIN GS-5).
V -> I (IN STRAIN GS-5).
V -> V (IN STRAIN GS-5).
D -> V (IN STRAIN GS-5).
S -> A (IN STRAIN GS-5).
S -> P (IN STRAIN GS-5).
S -> P (IN STRAIN GS-5).
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TSSGNWYYFGNDGYALIGWHVVEGRRVYFDENGYYRYASHD
ORNHWDYDYRRDFGRGSSSAVRFRHSRNGFFDNFFRF ->
HASILSLMVFRLRESSLQSVKVVSNTMILIFEMKFVIVM
(IN REF. 1)
13CB455A99A4FEC86 CRC64;
                        Score 100;
Pred. No. 7
                      Pred.
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Repeat; Dental
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I (IN STRAIN GS-5).

I (IN STRAIN MT4239).

V (IN STRAIN GS-5).

A (IN STRAINS GS-5 AND MT4467).

T (IN STRAIN GS-5).

PK (IN STRAINS GS-5, MT4239 AND
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I (IN STRAIN MT8148).
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1 VPSYSFARAHDSEVQDLIRDII

578 VPSYSFIRAHDSEVQDLIRNII 599

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537 VPNYVFIRAHDSEVQTRIAKII 558

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                          Matches
                         15;
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                                 Similarity
VPSYSFARAHDSEVQDLIRDII 22
                          Conservative
                          1;
                          Pred. No. 0.0
; Mismatches
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PACE CONSTRUCTION OF THE FERRICAL PROPERTY OF THE PROPERTY OF 
           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gilmore K.S., Russell R.R., Ferretti J.J.; "Analysis of the Streptococcus downei gtfS gene, glucosyltransferase that synthesizes soluble gluc Infect. Immun. 58:2452-2458(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-S precursor (EC 2.4.1.5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus downei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P29336;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco.hydro_70.
Pfam; PF0473; CW binding I; 8.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        +
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                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M30943; AAA26898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90316665; PubMed=2142479;
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                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = D-fructose + {(1,6)-alpha-D-glucosyl}(N+1).

ENZYME REGULATION: GLUCAN SYNTHESIS BY GTF-S IS INDEPENDENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMER GLUCAN UNLIKE GTF-I.
MISCELLANEOUS: GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECT. Immun. 58:2452-2458 (1990).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,6-GLUCOSE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6-glucosyltransferase)
                                                                                                   37
157
178
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                                                                                                                                                                                                                                                                                                                                                                                       Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Belongs to family 70 of glycosyl hydrolases. Contains 10 cell wall binding repeats.
                                                                                Ā
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; Lactobacillales; Streptococcaceae;
                  63.6%;
                                                                                  151590
                                                                                  ¥.
                                                                                                   CELL WALL
CATALYTIC
CATALYTIC
CATALYTIC
CELL WALL
                                       Score
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                                                                                  L WALL BINDING 10.
167296B5A2E8C476
                                                                                                                                                                                                                                                                                                      WALL BINDING 1. WALL BINDING 2.
                                                                                                                                                                                                                                                                                                                                                                                         Signal; Repeat; Dental caries
                  70;
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                 C (APPROXIMATE).
L BINDING 3.
L BINDING 4.
L BINDING 5.
L BINDING 6.
L BINDING 7.
L BINDING 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                         BINDING
                    0.0048;
                                       В
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                                         Length 1365;
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                                                                                     CRC64;
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  Gaps
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GTPD SEQUEN

GTPD SEARCH

AC P49331

AC P493
EMBL; M29296; AAA26895.1; -.
EMBL; D88653; BAA26103.1; -.
EMBL; D88656; BAA26107.1; -.
EMBL; D88659; BAA26111.1; -.
EMBL; D88662; BAA26115.1; -.
EMBL; D89979; BAA26121.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTFD STRMU
P49331; 069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-UA159 / ATCC 700610 / Serotype C;

MEDLINE=22295063; PubMed=12397186;

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Ajdic D., McShan W.M., McLaughlin R.E., Renton S., Jia H., Lin S.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,

Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti

Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular analyses of glucosyltransferase Streptococcus mutans."; FEMS Microbiol. Lett. 161:331-336(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRALIS | MT424|

MT4467 | Serotype E, and MT8148 |

MEDLINE=98231643; PubMed=9570124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the Streptococcus mutans the glucosyltransferase-S enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogen.";
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                                                                                                                                                                               entities requires a or send an email to
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-!- SIMILARITY: Contains 6 cell wall binding repeats.
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CRIALYTIC ACTIVITY: SUCKOSE + {(1,6)-alpha-D-glucosyl)(N) =
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                                                                                                                                                                                    equires a license agreement (S email to license@isb-sib.ch).
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PF02324; Glyco_hydro
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; IPR002479; CW binding.

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R01473; CW binding 1; 11.

R01473; CW binding 1; 11.
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KKKYTO -> EKEYTL (IN STRAIN MT4251).

A -> S (IN STRAIN MT4239).

TDQGSEA -> ADKGNDS (IN STRAIN MT4251).

TDQGS -> ADKGN (IN STRAINS MT4239 AND MT4245).

T -> A (IN STRAINS MT4239 AND MT4245).

T -> A (IN STRAINS MT4245 AND MT4251).

E -> K (IN STRAIN MT4251).

G -> R (IN STRAIN MT4251).

G -> R (IN STRAIN MT4245).

G -> R (IN STRAIN MT4239).

H -> Q (IN STRAIN MT4239).

Y -> C (IN STRAIN MT4239).

Y -> C (IN STRAIN MT4251).

F -> L (IN STRAIN MT4251).

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F -> L (IN STRAIN MT4251).

G -> P (IN STRAIN MT4245).

K -> T (IN STRAIN MT4245).

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R -> C (IN STRAIN MT4245).

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V (IN STRAIN MT4245).
T (IN STRAINS GS-5, MT-
1, MT4467 AND MT8148).
L (IN STRAIN MT4239).
N (IN STRAIN MT8149).
D (IN STRAINS MT4239, I
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1, MT4467 AND MT8148).

V (IN STRAINS GS-5, MT

1, MT4467 AND MT8148).

E (IN STRAIN MT4467).

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V (IN STRAINS MT4233).
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InterPro; IPR000766; GalP_Utransf_C.

InterPro; IPR005850; GalP_Utransf_N.

InterPro; IPR005849; GalP_Utransf_N.

InterPro; IPR005949; GalTZ.

InterPro; IPR005934; GalTZ.

INTERPAMS; IIGR01239; GalT_Z; 1.

INTERPAMS; IIGR01239; GALT_PUDP_TRANSF_II;

INTERPAMS; INTERPRO; INTERPRO; INTERPROSITE; PS01163; GALT_PUDP_TRANSF_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)
uridylyltransferase) (UDP-glucose--hexose-1-phosphate
uridylyltransferase).
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are nuse by non-profit institutions as long as its comparised and this statement is not removed. Usage entities requires a license agreement (See http://worsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-D-glucose 1-phosphate + U-l-pANTWAY: Galactose metabolism;
-!- SUBCELLULAR LOCATTON.
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Bacteria; Firmicutes
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Takami H., Takaki Y., Nakasone K.,
Hirama C., Fuji F., Masui N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., S.
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
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HAMAP; MF_00571; -;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extremophiles 3:227-233(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic analysis of halodurans C-125."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-450 FROM N.A. STRAIN=C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horikoshi K.;
                                                                                                                                    TIGRFAMS; TIGRO1239; gaIT_2; 1.
pROSITE; PS01163; GAL_P_UDP_TRANSF_II; 1.
Transferase; NucleotidyItransferase; Galactose metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic (Potential). SIMILARITY: Belongs to the galactose-1-phosphate uridylyltransferase family 2.
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 AHLHDSNVMDILRDEI
                          ARAHDSEVQDLIRDII
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JCM 9153;
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                                                                                                             57989
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56.2%;
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  475
                                                                                                             W.
                           22
                                                       2;
                                                                      Score 47;
Pred. No. 7
                                                                                                             16AF6F607FCEAE2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + UDP-galactose.
                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of alkaliphilic
                                                                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                DB
7.9;
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V., Kuhara S.
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•
                                                                                 Length 508;
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RESULT 8
                                                       STANDER REPRESENTATION OF THE PROPERTY OF THE 
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RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Bantier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Keft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Movella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Madueno E., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nacquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RY "Comparative genomics of Listeria species.";
Science 294,494-882 (2001).
C. -I- FUNCTION: The UvrABC repair system catalyzes the recognition and processing of DNA Lesions. UvrC both incises the 5' and 3' sides incision and the C-terminal half is responsible for the 3' incision and the C-terminal half is responsible for the 5' incision (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, C
10-OCT-2003 (Rel. 42, L
10-OCT-2003 (Rel. 42, L
UVRABC system protein C
UVRC OR LIN1197.
                                                                                                                                                                                                                                                                 Pfam; PF01541; Exci endo N; 1.
Pfam; PF02151; UVR; 1.
Probm; PD005870; UVR; C; 1.
SMART; SM00465; GIYC; I.
SMART; SM00278; HhH1; 1.
TIGREPMS; TIGR00194; UVrC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ListiList; LIN01197; -.

HAMAP; MF_00203; -; 1.

InterPro; IPR001363; HHH 1.

InterPro; IPR001943; UVTB/C.

InterPro; IPR001403; UVTC C.

InterPro; IPR000305; UVTC_N.
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STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q92CH5;
                                                       SEQUENCE
                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL596167; CAC96428.1;
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                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; AD1582; AD1582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the uvrC family. SIMILARITY: Contains 1 UVR domain.
                                                                                                                  response; excision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Interacts with uvrB in an incision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gimilarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                         PS50151; UVR; 1.
PS50164; UVRC_1; 1.
PS50165; UVRC_2; 1.
                                                       603 AA;
                                                                                           197
                                                                                    Excision nuclease;
Complete proteome.
97 232 UVR.
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                                                          69302 MW;
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Last annotation update)
C (UvrC protein) (Excinuclease ABC subunit
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                                                             8FA17669DB8EAFA1
                                                                                                                                                  DNA repair; DNA recombination;
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                                                             CRC64;
Length 603;
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Query Match

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RESULT
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                                                                                                                                        Hamap; MP_00203; -; I.
InterPro; IPR003583; HHH 1.
InterPro; IPR003583; UvrB/C.
InterPro; IPR001943; UvrC.C.
InterPro; IPR001962; UvrC.C.
InterPro; IPR001162; UvrC.C.
InterPro; IPR000305; UvrC.N.
Pfam; PF02151; UVR; 1.
Pr0Dom; PD005870; UVrC.C; 1.
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Q8Y7F0;
10-OCT-2003 (Re
10-OCT-2003 (Re
10-OCT-2003 (Re
UVIABC BYSTEM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Gcience 204.840.857(2015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 294:849-852(2001).

-I- FUNCTION: The UVYABE repair system catalyzes the recognition processing of DNA lesions. UVrC both incises the 5' and 3' si of the lesion. The N-terminal half is responsible for the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the uvrC fav-!- SIMILARITY: Contains 1 UVR domain.
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TIGRFAMS; TIGR00194; UVTC; 1. PROSITE; PS50151; UVR; 1. PROSITE; PS50164; UVRC_1; 1.
                                                                                     SMART; SM00465; GIYC; 1.
SMART; SM00278; HhH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; AB1229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL591978; CAC99312.1;
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incision (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation updat
em protein C (UvrC protein) (Exc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AB1229.
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                                                                                                                      UvrC_C; 1.
IYc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.5%;
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(UvrC protein) (Excinuclease ABC
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uvrC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for the
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Watanabe A., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
(EC 2.1.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50165; UVRC_2; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BC 2.1.1.-).
UBIE OR MLR3165.
Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98GV1;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA excision;
DOMAIN 1
                                                   HAMAP, MF 01813; ; 1.
InterPro; IPR001601; Methyltransf.
InterPro; IPR000051; SAM bind.
InterPro; IPR004034; Ubi_Men Metransf.
InterPro; IPR004033; UbiE/COQ5 Metrf.
Pfam; PF01209; Ubie_methyltran; 1.
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesorhizobium loti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                             entities requires a license agreement (See or send an email to license@isb-sib.ch).
                        PROSITE; PS01183; PROSITE; PS01184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome structure
                                                                                                                                                EMBL; AP003001; BAB50115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 2-polyprenyl-6-
methoxy-1,4-benzoquinol = S-adenosyl-L-homocysteine + 2-
                                                                                                                                                                                                                                                                                                                     s-adenosyl-L-homocysteine + menaquinol.
PATHWAY: Menaquinone biosynthesis; last
PATHWAY: Ubiquinone biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DMKH2) to menaquinone (MKH2) and the conversion of 2-polyprenyl-6-methoxy-1,4-benzoquinol (DDMC 2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol (DMQH2) (I
                                                                                                                                                                                                                                                                                                                                                                   polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol.
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol
                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHILO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRSY-FSGTHDSKTORLVQEIV 62
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(Rel. 42, Last seq
(Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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197 232 UV
           biosynthesis;
                        Ubie methyltran;
83; UBIE 1; 1.
84; UBIE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69315 MW;
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45.5%;
1.
Ubiquinone biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6,
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Pred. No. 1
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                                                                                                                                                                                             http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                      step.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               о́ ».,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DDMQH2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H., Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E., Marino C.L., Gilloti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Marino C.L., Gilloti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V., God Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi I.T., Ge Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C., Kishi J.T., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C., Kishima J.D., Kitaiima J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCSP XYLFT
Q87DR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methyltransferase; SEQUENCE 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glycine dehydrogenase [decarboxylating] (EC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XYLFT
                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 185:1018-1026(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Civerolo B.L.,
Kitajima J.P.;
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease and citrus variegated chlorosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCVP OR PD0620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22421331; PubMed=12533478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kylella fastidiosa (strain
                                                  HAMAP; MF_00711; -; 1.
InterPro; IPR003437; GDC-P
Pfam; PF02347; GDC-P; 1.
                                                                                                        EMBL; AE012555; AA028492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fastidiosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative analyses of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L0-OCT-2003
                                                                                                                                                                                                                                                                                                                FUNCTION: The glycine cleavage system catalyzes the degradat: glycine. The protein binds the alpha-amino group of glycine through its pyridoxal phosphate cofactor; CO(2) is released the remaining methylamine moiety is then transferred to the lipoamide cofactor of the H protein (By similarity). CAPALIYIC ACTIVITY: Glycine + lipoyiprotein = S-aminomethyldihydrolipoylprotein + CO(2). COPACTOR: Pyridoxal phosphate (By similarity). SUBUNIT: The glycine cleavage system is composed of four prosuments.
                                                                                                                                                                                                                                                                               P, T, L and H (By similarity).
SIMILARITY: Belongs to the govp family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSFARAHDSEVODLIRDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Glycine cleavage system P-protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
28291 M
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42.1%;
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MW; 99096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Temeculal / ATCC 700964)
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9909682B726B2828 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome sequences of Pierce's is strains of Xylella
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycine
                                                                                                                                                                                                                                          a collaboration -
MBL outstation -
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                                                                                                                                                                                                                                                                                                                           proteins:
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                                                                                                                                                                                                                                      outstation
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Oxidoreductase; Pyridoxal phosphate; Complete proteome:
BINDING 715 715 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

BINDING

993

107646 MW;

BCC04E829C442F43

CRC64

1;

Length 993;

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Matches 7
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Best Local
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3_DROME STANDARD
P04373;
P04373;
P04373;
P04373;
Rel. 04, C
20-MAR-1987 (Rel. 04, C
20-MAR-2087 (Rel. 04, L
28-FEB-2003 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-85061628; PubMed-6209583;

MEDLINE-85061628; PubMed-6209583;

Matsuo Y., Inouye S., Yoshioka K.,

Matsuo Y., Inouye S., Yoshioka K.,

"Identification of the coding sequence for a reverse
transcriptase-like enzyme in a transposable genetic elements."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haraboda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last annotation update)
Retrovirus-related Pol polyprotein from transposon 17.6 (Contains:
Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49);
                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.";
Nature 312:659-661(1984).
-|- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endonuclease].
                                                                                                                                Endonuclease;
ACT_SITE
                                                                                                                                                            Hydrolase; Aspartyl protease;
                                                                                                                                                                         Pfam; PF00077; rvp; 1.
Pfam; PF00078; rvt; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
                                                                                                                                                                                                                   InterPro; IFR001969; Aspprocease_AS.
InterPro; IFR003907; Pept A acid.
InterPro; IFR001995; PeptIdase_A2.
InterPro; IFR001584; Rve.
InterPro; IFR000477; RVTse.
Pfam; PF00665; rve; 1.
                                                                                                                                                                                                                                                                                                                         EMBL; X01472; CAA25702.1; -. PIR; A03971; GNFF17.
MEROPS; A02.052; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- MIŚCELĹANEOUS: The open reading frame is located in a copia-like
transposable element called 17.6.
                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0014453; 17.6\pol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         969
213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {DNA} (N).
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                          4
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8; Conserv
                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPVEAYXEXGDSEIQDLIEE 988
 YSYPOAYEQEVESQIQDML
                          YSFARAHDSEVQDLIRDII
                                                                                                                  1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                          Conservative
                                                                                                                                partyl protease; RNA-directed DNA polymerase;
Transferase; Polyprotein; Transposable element.
30 30 PROTEASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.9%;
                                                                                                                  30 PRO
122697 MW;
                                                                     40.9%;
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                                                          8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB Pred. No. 35;
                                                                     Score 45;
Pred. No.
                           22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                          Mismatches
                                                                                                                   C893F5C4A7E1F091
                                                                          38;
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                                                          4
                                                                                    Length 1058;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yuki
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                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                            0;
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YH75 IID AC DT DT DT DT

YH75 ARCFU 028499; 16-0CT-2001 16-0CT-2001

STANDARD;

A

16-0CT-2001 Hypothetical

(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
L protein AF1775.

update)

RESULT 14

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SYE_STAP
ID SYE S

AC QBCTU
DT 10-00
CC -1- CC
CC -1-
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k Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.
A Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Che
A Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
"Genome-based analysis of virulence genes in a non-biofilm-
"Staphylococcus epidermidis strain (ATCC 12228).";
I Mol. Microbiol. 49:1577-1593(2003).
L Mol. Microbiol. 49:1577-1593(2003).
C -- CATALYTIC ACTIVITY: ATP + L-Glutamate + tRNA(Glu) = AMP
C -- CATALYTIC MOLOMET (By similarity).
C -- SUBUNIT: MOLOMET (By similarity).
                                                                                                          Matches
                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00022; -; 1
InterPro; IPR004527; Gltx_bact.
InterPro; IPR009524; Glt_tRNA-synt_lc.
InterPro; IPR008925; tRNA-synt_bind.
InterPro; IPR008925; tRNA-synt_l.
InterPro; IPR001412; tRNA-synt_l.
Pfam; PF00749; tRNA-synt_lc; 1
PRINTS; PR00987; TRNASYNTHGLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8CTU3;
10-OCT-2003
10-OCT-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=ATCC 12228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epiderm Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLTX OR SE0290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutamyl-tRNA synthetase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE016744; AA003887.1; -.
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                               Complete
                                                                                                                                                                                                                                                                                                                                                        TIGRFAMB; TIGR00464; gltX_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STABP
193
                                                                                                          10;
                                                   --
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                               proteome.
VPTYNFAVAVDDHYMQISDVIR 214
                                                VPSYSFARA---HDSEVQDLIR 19
                                                                                                                                                                                                                 252
255
484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation updat
(Rel. 42, Last annotation (Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermidis.
icutes; Bacillales;
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                                                                                                                                                                                                                                              256
255
255
                                                                                                                                                                                                                       56370
                                                                                                                                 40.5%;
                                                                                                                                                                                                                 "KMSKS" REGION.
ATP (BY SIMILARITY)
MW; 644A72F0C8B24FEB
                                                                                                             υ
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                                                                                                          Score 44.5; I
Pred. No. 19;
5; Mismatches
                                                                                                                                                                                                                                                                                                        "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
) (Glutamate--tRNA ligaве)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   es in a non-biofilm-forming 12228).";
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                                                                                                                                                                1;
                                                                                                                4.
                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                   Length 484;
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Chen
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AF1775.

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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P17342;
01-AUG-1990
28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- SIMILARITY: Belongs to the ATZ/TRZ family.
receptor.
Nucleic A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEMENT TO SEND THE PROPERTY OF THE PROPERTY OF SEND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Atrial natriuretic peptide clearance receptor precursor (ANP-C)
(ANPRC) (NPR-C) (Atrial natriuretic peptide C-type receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR;
                                                                                                           "cDNA sequence of the
                                                                                                                                                       MEDLINE=90287735; PubMed=2162522; Lowe D.G., Camerato T.R., Goeddel
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPR3 OR ANPRC
                                                                                                                                                                                                                                   TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR006680; Amidohydro_1.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F69471; F69471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF1775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE000980; AAB89475.1; -.
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                                           Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSFARAHDSEVODLIRDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYSSARDHDLKLMEEVREI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       il protein, Hydrolase, Complete
330 AA, 37069 MW, 525AD9F7F35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                           18:3412-3412(1990)
                                                                                                                                                                                                                                                                           (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%;
                                                                                                                       human
                                                                                                                   Goeddel D.V.;
an atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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525AD9F7F35A6FB1 CRC64;
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Query Match
Best Local Similarity
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-I- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWITH GIANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULARION MUTHOUT A ROLE IN SIGNAL TRANSDUCTION.
-I- SIMILARITY: TO ANP-A AND ANP-B RECEPTORS IN THEIR EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1997) to the EMBL/G-1- FUNCTION: RECEPTOR FOR ATRIAL GUANYLATE CYCLASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lens epithelium;
Rae J.L., Shepard A.R.;
"Human lens epithelial mRNA for atrial natriuretic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide clearance receptor cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porter J.G., Arfsten A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90386656; PubMed=2169733;
                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
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EMBL; M59305; AAA51734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004872; F:receptor activity; TAS: GO; GO:0001501; P:skeletal development; T InterPro; IPR001128; ANF_receptor. InterPro; IPR001170; Ntpep_receptorN. Pfam; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:7945; NPR3.
                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00255; NATPEPTIDER.
PROSITE; PS00458; ANF_RECEPTORS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1JDN; 05-SEP-01
                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer; disulfide-linked.
SUBCELLULAR LOCATION: Type I membrane
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108962;
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                                                                                                                                                                                                                                                                                                                                        Glycoprotein;
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
     Score
Pred.
                                                                        SG -> C (i)
/FTId=VSP_
                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                   RECEPTOR.

EXTRACELLULAR (POTENTIAL).
                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                        ATRIAL NATRIURETIC PEPTIDE
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                                                     G -> C (in isoform 2).
FTId=VSP_001812.
8A66415F7F7D62B7 CRC64;
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       No.
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26;
                                                                                                                                                                                                                                                                                                                                            Signal; Alternative
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                        Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregory L.C.,
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                                                                                            <u>2</u>:
                                                                                                               (POTENTIAL)
                                                                                                                                 (POTENTIAL).
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MBL outstation -
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Matches
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-!- DOMAIN: CONSISTS OF FIVE MODULES WITH TWO EPIMERIZATION DOMAINS IN THE SECOND AND FOURTH MODULES, AND A PUTATIVE C-TERMINAL THIS SECOND AND FOURTH MODULES, AND A PUTATIVE C-TERMINAL THIOSSTERASE DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVLDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION, CONDENSATION METATALISM (OPTIONAL).

N METATLATION (OPTIONAL).

N METATLATION (OPTIONAL).

N MISCELLANEOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC DODECAPEPTIDE, THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST ABUNDANT IS BACITRACIN A, BRANCHED CYCLIC DODECAPEPTIDE. IT CONTAINS AN N-TERMINAL LINEAR PENTAPEPTIDE MODIETY (ILE-CYS-LEU-D-PRODUCT AND A C-TERMINAL HIPSTAPEPTIDE RING (LYS-D-ORN-ILE-D-PHE-HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE C-TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE. IT CONTAINS FOUR AMINO ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7, PHE-9, AND ASP-11)
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bacitracin synthetase 3 (BA3) [Includes: ATP-dependent isoleucine adenylase (IleA) (Isoleucine activase); ATP-dependent D-phenylalanine adenylase (D-phen) (D-phenylalanine activase); ATP-dependent histidine adenylase (HisA) (Histidine activase); ATP-dependent D-aspartate adenylase (D-AspA) (D-aspartate activase); ATP-dependent asparagine adenylase (AsnA) (Asparagine activase); ATP-dependent asparagine adenylase (AsnA) (Asparagine activase); ASpartate racemase (EC 5.1.1.13); Phenylalanine racemase (ATP hydrolyzing)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=98089193; PubMed=9427658;
KONZ D., Klens A., Schoergendorfer K.,
"The bacitracin biosynthesis operon of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10716:
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SUBUNIT: LARGE MULTIENZYME COMPLEX OF BA1, BA2 AND BA3.
DOMAIN: CONSISTS OF FIVE MODITIES OF THE M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUNCTION: INDUCES PEPTIDE SYNTHESIS, ACTIVATES AND INCORPORATE FIVE AMINO ACIDS, FORMS A THIAZOLINE RING BETWEEN THE FIRST TY AMINO ACIDS AND INCOPORATES A D-GLUTAMINE IN THE FOURTH POSITION ACTIVITY: L-aspartate = D-aspartate.

CATALYTIC ACTIVITY: ATP + L-phenylalanine = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenylalanine.
COFACTOR: Contains 5 covalently bound phosphopantetheines
                                                                                                                                                                                                                                                                                                                                         PHE-9, AND ASP-11).
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                             SIMILARITY: Contains 5 acyl carrier domains.
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of Bacillus licheniformis ATCC
multi-modular peptide
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RESULT 17
SYE STAAM
ID SYE STAAM
AC Q99W75;
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ACCOMPANDACTOR OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      片
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Best Local &
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28-FEB-2003
28-FEB-2003
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DOMAIN
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PROSITE; PS50075; ACP_DOMAIN; 5.

Ligase; Isomerase; Hydrolase; Antibiotic biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00501; AMP-binding; 5.
Pfam; PF00568; Condensation; 7.
Pfam; PF00550; pp-binding; 5.
Pfam; PF00975; Thioesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001242; Condensatn.
InterPro; IPR006163; Pp_bind.
InterPro; IPR006162; Ppantne_S.
InterPro; IPR001031; Thioesterase.
                    Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Kuroda M., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama Mizutami-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shattori M., Ogasawara N., Haysahi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLTX OR SAV0528 OR SA0486 OR MW0483.
Staphylococcus aureus (strain Mu50 /
Staphylococcus aureus (strain N315),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glutamyl-tRNA
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Mu50 / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=158878,
  "Whole genome sequencing
aureus.";
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; P14687; 1AMU.
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation)
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ilarity 45.5%;
Conservative
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ACYL CARRIER (ACP) 3
ACYL CARRIER (ACP) 4
ACYL CARRIER (ACP) 5
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PHOSPHOPANTETHEINE (
PHOSPHOPANTETHEINE (
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DOMAIN 2
DOMAIN 3
DOMAIN 4
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Pred. No.
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L CARRIER (ACP) 2.
L CARRIER (ACP) 3.
L CARRIER (ACP) 4.
L CARRIER (ACP) 5.
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1 (ISOLEUCINE-ACTIVATING).
2 (D-PHENYLALANINE-ACTIVATING).
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(D-ASPARTIC ACID-ACTIVATING)
(ASPARAGINE-ACTIVATING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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(BY SIMILARITY).
(BY SIMILARITY).
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(BY SIMILARITY).
                                      Staphylococcus
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Ito T.,
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                                                                                                 Shiba
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-2DPAGE; Q99W75; STAAN.
HAMAP; MF Q0022; -; 1.
InterPro; IPR004527; GltX bact.
InterPro; IPR00922; Glu TRNA-synt 1c.
InterPro; IPR008925; tRNA-synt bind.
InterPro; IPR008412; tRNA-synt 1.
InterPro; IPR001412; tRNA-synt 1c; 1.
Pfam; PP00749; tRNA-synt 1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
                                                                                                                                                                                                                                                                                                                                                                                STRR6
                                                                                                                                                                                                                                                  Q8CWN5;
10-OCT-2003
10-OCT-2003
10-OCT-2003
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Nagai Y., Iwama N., Asano K., Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP003359; BAB56690.1; -.
EMBL; AP003130; BAB41716.1; -.
EMBL; AP004823; BAB94348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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[2]
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-!- CATALYTIC ACTIVITY: ATP + L-glutamate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22040717;    PubMed=12044378;
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HSSP; P27000; 1GLN.
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                                                                      Streptococcus.
NCBI_TaxID=171101;
                                                                                                                          Streptococcus pneumon Bacteria; Firmicutes;
                                                                                                                                                                            GLTX OR SPR1881.
                                                                                                                                                                                                                             Glutamyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
     SEQUENCE FROM N.A. MEDLINE=21429245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in the content is in the content in the content is in the content in the content is in the content in the content is not removed. Usage by and for content is not removed.
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SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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                                                                                                                                                                                                                                                                                                                                                      STRR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193
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9; Conserv
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                                                                                                                                                                                                                                                  (Rel.
(Rel.
(Rel.
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                                                                                                                                                    pneumoniae
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                                                                                                                                                                                              42, Created)
42, Last sequence update)
42, Last sequence update)
42, Last annotation update)
42hetase (BC 6.1.1.17) (Glutamate--tRNA ligase)
       PubMed=11544234;
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Lactobacillales;
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ATP (BY SIMILARITY).
MW; 4CBASFF08DA23EFA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43.5;
Pred. No. 2
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imi T., Kuroda H., Cui L.,
                                                                                                                                                    ATCC BAA-255 / R6).
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                                                                                                                               Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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RANGE REPRESENTATION OF THE PROPERTY OF THE PR
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InterPro; IPR004527; Gltx_bact.
InterPro; IPR00924; Glu ENNA-synt lo.
InterPro; IPR008925; tRNA-synt_bind.
InterPro; IPR008925; tRNA-synt_1.
InterPro; IPR001412; tRNA-synt_1.
PEAM; PP00749; tRNA-synt_1.; 1.
PRINTS; PR00987; TRNASYNTHGLU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SUBUNIT: Monomer (By similaritan)
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hexose transporter HXT14.
HXT14 OR HXT9 OR YMJ318C OR N0345.
Saccharomyces cerevisiae (Baker's Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycees.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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PIR; F98106; F98106.
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                          MEDLINE=9607632; PubMed=7502583; Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.; Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.; ensequencing analysis of a 24.7 kb fragment of yeast chromosome identifies six known genes, a new member of the hexose transpor
                                                                                                                                       SEQUENCE FROM N.A. STRAIN=S288C / FY1
                                                                                                                                                                                                                       NCBI_TaxID=4932;
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family and
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486 AA;
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ATP (BY SIMILARITY)
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Pred. No. 40;
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InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar transpt.
pfam; PF00083; sugar tr; 1.
PRINTS; PR00171; SUGRIRNSPORT.
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EMBL; Z71595; CAA96250.1; -.
PIR; S63299; S63299.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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PROSITE; PS00217; SUGAR_TRANSPORT_2.
PROSITE; PS00217; SUGAR_TRANSPORT; T.
Repeat; Transmembrane; Sugar_transport; T.
PROPERSY T.
PR
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3; Mismatches
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2 (POTENTIAL).
CYPTORY ACCURATE AND A CONTROL OF A CONTRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 540;
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RESULT 21
YIBQ HAEIN
ID YIBQ HAEIN
AC P44863;

STANDARD;

PRT;

280

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Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U1413; AAA21385.1; -
EMBL; Z49305; CAA89321.1; -
PIR; S48302; S48302.
HSSP; Q13257; 1DUJ.
Germonline; 141645; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWEL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assembled spindles from leaving mitosis
-!- SUBUNIT: The spindle checkpoint complex
and MADJ. It interacts with CDC20.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE MADZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Budding yeast Cdc20: a target of the spindle checkpoint."; Science 279:1041-1044(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98128031; PubMed=9461437;
Hwang L.H., Lau L.F., Smith D.L.,
Hwang E.S., Amon A., Murray A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pohl T.M., Aljinov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li R., Havel C., Wate
Submitted (AUG-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Last annotation update)
Mitotic spindle checkpoint component MAD2 (Mi
MAD2 OR YJL030W OR J1256
                                                                                                                                                                                                                                   SGD; S0003567; MAD2.
GO; GO:0000778; C:condensed nuclear chromosome kinetochore;
GO; GO:0005643; C:cunclear pore; IDA.
GO; GO:0007094; P:mitotic spindle checkpoint; IGI.
InterPro; IPRO03511; DNAbind_HORMA.
Pfam; PF02301; HORMA; 1.
PROSITE; PS50815; HORMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 66:519-531(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: Feedback control that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li R., Murray A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91330300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                            Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - |- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Feedback control of mitosis in budding yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTIONS
49
                                        8
                                                                                      Similarity 7; Conser
                                      RAHDSEVODLIRDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aljinovic
                                                                                                                                                                        196 AA;
                                                                                                                                                                                                                 Mitosis; Nuclear protein.
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contains 1 HORMA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson
.994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1651172;
                                                                                                                                                                        22284 MW;
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the E
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    63
                                             22
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                                                                                        4
                                                                                                                                                                          HORMA.
; EFE59916C5720644 CRC64;
                                                                                                           Score 42;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mistrot C.A., Hardwick K.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevents cells with incompletely mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex is composed of MAD1, MAD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           moved. Usage by and fo
(See http://www.isb-sib.
                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mitotic MAD2 protein)
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                                                                                                                               Length 196;
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                                                                                           Gaps
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Last sequence update)

Created)

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RESULT 22
TF3A_YEAST
   TAPETER SOOS
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                                                                                                                                                                                                                                                                                                                             Query Match
 19933;
1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transcription factor IIIA (TFIIIA)
TROZ OR PZFI OR TFIIIA OR YPRIBGC OR P9677.9.
Saccharomyces cerevisiae (Baker's yeast)
Saccharomyces cerevisiae (Baker's yeast)
Saccharomyces (Baccharomycetes; Saccharomyces)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Doughterty B.A., Merrick J.M. McKenlavage A.R., Bult C.J., Tizhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weidman J.F., Phillips C.A., Spriggs T., Baudek D.M., Brandon R.C. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Grahm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Rd / KW20 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein HI0755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electrophoresis 21:411-429(2000).
-!- SIMILARITY: STRONG, TO E.COLI YIBQ.
                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Langen H., Takacs B., Evers S., Berndt F., Lanm n.m., mipt L., Gray C., Fountoulakis M., "Two-dimensional map of the proteome of Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20137488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
                                                                                                                                                        TF3A_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole-genome random sequencing
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                           PF04748; div_psaccdeacet; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U32759; AAC22414.1; ALT_INIT.
                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                 1 VPSYSFARAHDSEVQDLIRDII 22
:|::|||::|||::
59 IPAAPYARARNQEAKSQGRDIL 80
                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20137488; PubMed=10675023;
I., Takacs B., Evers S., Berndt P.,
Fountoulakis M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR006837; DUF610.
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                             280 AA;
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                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,
41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCC 51907;
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30740
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                                                                                                                                                                                                                                                                                                                                                           WW;
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                                                                                                                                                                                                                                                                                                               Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                               PROTEIN HI0755.
; C739E021613B53B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assembly of Haemophilus influenzae
                                                                                                                                                            429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayton R.A., Kirkness E.F., Dougherty B.A., Merrick J.M.,
                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                                  8;
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                                                                                                                                                                                                                                                                                                                                Length 280
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RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Ra Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Rabotstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Ra Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Ra Botstein D., Bowman S., Bruckner M., Cotter F., Davis K., Davis R.M., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Ra Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Ra Duncan M., Floeth M., Fortin N., Fritz C., Goffeau A., Ra Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W., Ra Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W., Ra Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Ra Komp C., Kurdi O., Labhari D., Lew H., Lin A., Lin D., Louis E.J., Ra Mcaller-Auer S., Namath A., Nentwich U., Oeffner P., Pearson D., Ra Mcaller-Auer S., Namath A., Nentwich U., Oeffner P., Pearson D., Ra Mcaller-Auer S., Schramm S., Schroeder M., Sdicu A.M., Tettelin H., Ra Mcaller B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H., Ra Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Valere 387:103-105(1997).

T. "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:103-105(1997).

T. Approximately 50 Bases WITHIN THE SS RNA GENES, SI SREQUIRED FOR CRARECT TRANSCRIBED 5S RNA'S.

C. INDS THE TRANSCRIBED 5S RNA'S.
                                                                                                                                                                 TRANSFAC; 103-17;
SGD; S0006390; PEPFI.
SGD; GO:0005667; C:transcription factor complex; IPI.
GO; GO:0005667; C:transcription factor act.
GO; GO:0003709; F:RNA polymerase III transcription factor act.
GO; GO:0003709; F:transcription initiation from Pol III promote
InterPro; IPR007087; Znf C2H2.
Pfam; PP00096; Zf-C2H2; 9.
SMART; SM00355; ZnF C2H2; 9.
PROSITE; PS00028; ZINC_FINGER C2H2_1; 8.
PROSITE; PS00157; ZINC_FINGER C2H2_2; 6.
Transcription regulation; Zinc_Finger; Metal-binding; DNA-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woychik N.A., Young R.A.; "Genes encoding transcription factor IIIA and the RNA polymerase common subunit RPB6 are divergently transcribed in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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MEDLINE=97313271; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92237295;
Woychik N.A., Your
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces
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DOMAIN
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M80611; AAB08014.1; -.
EMBL; M90638; -; NOT_ANNOTATED_CDS.
EMBL; U25841; AAB64615.1; -.
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GermOnline; 144451; -.
     Transcription regulation; Zin
Transcription regulation; Zin
RNA-binding; Repeat; Nuclear
DOMAIN
24
32N FING
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ZN_FING
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                     SER-RICH.
C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions ong as its content is in yed. Usage by and for content is the content of the content 
                                                                                                                                                                                                                                  Metal-binding; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter; IPI.
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RESULT 23
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Best Local S
Matches 10
InterPro; IPR000722; RNA pol A.
InterPro; IPR007080; RNA pol Rpbl 1.
InterPro; IPR007080; RNA pol Rpbl 3.
InterPro; IPR007083; RNA pol Rpbl 4.
InterPro; IPR007081; RNA pol Rpbl 5.
InterPro; IPR006592; RNA pol Rpbl 1; 1.
Pfam; PF04997; RNA pol Rpbl 2; 1.
Pfam; PF04983; RNA pol Rpbl 3; 1.
Pfam; PF04983; RNA pol Rpbl 4; 1.
Pfam; PF04989; RNA pol Rpbl 4; 1.
Pfam; PF04998; RNA pol Rpbl 5; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-NCFB 2973;

MEDLINE-97016803; PubMed-8863429;

MORSE R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;

Morse R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;

"Analysis of the beta' subunit of DNA-dependent RNA polymerase does not support the hypothesis inferred from 16S rRNA analysis that Oenococcus oeni (formerly Leuconostoc oenos) is a tachytelic (fast-evolving) bacterium.";

(fast-evolving) bacterium.";
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Bacteria; Firmicutes; Lactobacillales; Weissella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-directed beta' chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              {RNA}(N).
SUBUNIT: The
enzyme which
                                                                                                                                                                                                                                                                                                                                                                         . J. Syst. Bacteriol. 46:1004-1009(1996).
FUNCTION: DNA-dependent RNA polymerase cataly:
of DNA into RNA using the four ribonucleoside
                                                                                                                                                                                                                                                                                   beta' chain.
SIMILARITY: Belongs to the RNA polymerase beta' chain family.
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Q9KWU6; 1HQM.
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(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
d RNA polymerase beta' chain (EC 2)
(RNA polymerase beta' subunit) (
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Pred. No.
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2 alpha
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a chains,
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Q63425;
01-NOV-1997
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NON_TER 1 1 1 1
NON_TER 1046 1046
SEQUENCE 1046 AA; 117107 MW
                                                                                                                                                                                                                                                                                                                     targeted in Schwann cells.";
J. Biol. Chem. 273:5794-5800(1998)
-I- FUNCTION: Seems to be required
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Mammalia; Butheria;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                              result of alternative intron retention and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                possible role in axonal Neuron 12:497-508(1994).
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Periaxin.
         +++
                                                                                                                                                                                                                                                                                                                                                                                     Dytrych L., Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 1364-1371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94206531; PubMed=8155317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Wistar;
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                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98157980; PubMed=9488714;
                                                                                                                                                                                                                                    Biol. Chem. 273:5794-5800 (1998).

FUNCTION: Seems to be required for maintenance of peripheral nerwingelin sheath. May have a role in axon-glial interactions, possibly by interacting with the cytoplasmic domains of integral membrane proteins such as myelin-associated glycoprotein in the periaxonal regions of the Schwann cell plasma membrane. May have role in the early phases of myelin deposition.
         DOMAIN: The Arg/Lys-rich basic domain funct
nuclear localization signal.
PTM: The N-terminus is blocked.
SIMILARITY: Belongs to the periaxin family.
SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                              Name=2; Synonyms=S-periaxin;
IsoId=063425-2; Sequence-VSP 004368,
TISSUE SPECIFICITY: NEURONES, SCHWANN
DEVELOPMENTAL STAGE: MRNA AND PROTEIN
NERVE BETWEEN POSNATAL DAYS 8 AND 20;
                                                                         DOMAIN: Has a remarkable domain of sometimes followed by a tripeptide functional basic and acidic domains
                                                                                                                                                                                                 Name=1; Synonyms=L-periaxin; IsoId=Q63425-1; Sequence=Displayed;
                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                              ych L., Sherman D.L., Gillespie C.S., Brophy P.J.;
PDZ domain proteins encoded by the murine periaxin gene
lt of alternative intron retention and are differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 HDEDVMDVLEDVI 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEP-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.S., Sherman D.L., Blair G.E., a novel protein of myelinating ole in axonal ensheathment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rat).
Da; Chordata;
.a; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35, Created)
41, Last sequence update)
41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D54C62C26A7F1696 CRC64;
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О
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                        repetitive spacer, it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e+02;
                                                                                                                                 8, VSP_004369;
N CELL-SPECIFIC.
N LEVELS PEAK IN :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brophy P.J.
Schwann cel
                                                                  functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1046;
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                                                                                           pentameric may separat
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RESULT
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PROBLEM REPORT OF THE PROBLEM OF THE
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Best Local Similarity
Matches 6; Conserv
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DOMAIN 16 85
DOMAIN 136 139
DOMAIN 118 196
DOMAIN 208 211
DOMAIN 432 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z29649; CAA82757.2;
InterPro; IPR001478; PDZ;
Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vi-vi-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Urea amidolyase [Includes: Urea carboxylase (EC 6.3.4.6); Allophanate
hydrolase (EC 3.5.1.54)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P32528;
                                                                                                                                                                                        Rieger M.;
Submitted
                                                                                                                                                                                                                                                                                       MEDILINE=92199240; PubMed=1802034; Genbauffe F.S., Cooper T.G.; "The urea amidolyase (DUR1,2) genupa Seq. 2:19-32(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                            SEQUENCE OF 873-1835 FROM N.A.
    MEDLINE=93377417;
                   SEQUENCE OF 1487-1835 FROM N.A. STRAIN=S288c;
                                                                                     Feldmann H., Mannhaupt G., S
Submitted (AUG-1994) to the
                                                                                                                           STRAIN-S288c;
                                                                                                                                                                                                                                  STRAIN=S288c;
                                                                                                                                                                                                                                                   SEQUENCE OF 1-893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1001 MPSFGLSRGKEAEIQD 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z29649; CAA82757.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 OR YBR208C OR YBR1448
                                                                                                                                                                                                                                                                                                                                                                                                                          TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ш
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128
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                                                                                                                                                                                        (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
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147
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                                                                                                                                                                                                                                                          FROM N.A.
        PubMed=8368014;
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                                                                                     Schwarzlose C., Vetter I.;
e EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIQSLSPVKKKKMVIGTLGT -> VRVLSPVPVQDSPSDAV
AAP (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 1;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 APPROXIMATE TANDEM
[LIVMAG]-P-[ED]-[LIVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RG/LYS-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FF6593BCFA23A437 CRC64;
                                                                                                                                                                                                                                                                                                                            of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1835 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ×
                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 004369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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Yeast 9:797-806(1993).
                                                                                                                                                                                                    pfam; pF02682; AHS1; 1.
pfam; pF02682; AHS1; 1.
pfam; pF01425; Anidase; 1.
pfam; pF01425; Anidase; 1.
pfam; pF01425; Anidase; 1.
pfam; pF002785; Biotin_Lipoyl; 1.
pfam; pF00284; biotin_Lipoyl; 1.
pfam; pF00284; CP8ase_L_chain; 1.
pfam; pF00286; CP8ase_L_D2; 1.
pR0SITE; pS00188; BIOTIN; 1.
pR0SITE; pS00866; CPSASE_1; 1.
                                                          Query Match
Best Local (
                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Hydrolysis of
-!- CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001882; I
InterPro; IPR005482; I
InterPro; IPR000089; I
InterPro; IPR005479;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Germonline; 138751; -.
SGD; S0000412; DURL,2.
GO; GO:0004039; F:aallophanate hydrolase activity; IMP.
GO; GO:0004847; F:urea carboxylase activity; IMP.
GO; GO:000487; F:urea metabolism; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M64926; AAC41643.1; -.
EMBL; Z36077; CAA85172.1; -.
EMBL; Z21487; CAA79695.1; -.
PIR; S46082; S46082.
                                                                                           CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005481; InterPro; IPR003778; InterPro; IPR003833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P24182; 1BNC.
                                                                                                                                                                                          Ligase;
Biotin;
                                                                                                                                                                                                                                                                                                                                                                                                                            [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carboxylate.
CATALYTIC ACTIVITY: Urea-1-carboxylate + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Allantoin and arginine metabolism SUBUNIT: Monomer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDUCTION: By allophanate or its non-metabolized analog oxalurate. Repressed in the presence of readily used ni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sources.
  102
                         N
                                              Similarity
7; Conserve
                                                                                                                                                                                             ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                              IPR0001
 PSFAYEPSKDSKVVELLRN
                      PSYSFARAHDSEVQDLIRD
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96
256
459
830
1395
1835
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                                                Conservative
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1798
96
258
459
430
1395
                                                                                                                                                                                                                                                                                                                                                     Biotin_carb_C.
Biotin_lipoyl.
CPase_L_D2.
CPase_L_N.
DUF183.
                                                                                                                                                                                                                                                                                                                                                                                                                  Biotin_BS
                                                                                                                                                                                                                                                                                                                                             DUF213.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Amidase
                                                            36.8%;
                                                                                                201831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  urea to ammonia and + urea + CO(2) = ADP
                                                                                                  P -> R (IN REF. 1).

LKX -> KXN (IN REF. 1).

I -> M (IN REF. 1).

E -> K (IN REF. 1).

D -> E (IN REF. 1).

MW; F52BODDOFE42CD65
                                                                                                                                                            BIOTIN.
                                                    8
                                                              Score
Pred.
                           20
                                                                                                                                                                                     ATP (POTENTIAL).
                                                    Mismatches
                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome II of the DUR1,2
                                                                   2.le+02;
                                                                            DB 1;
                                                                                                                                                   REF. 1).
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                                                                                                                                                                                                             Arginine metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP
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                                                                             Length 1835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate + urea-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMP.
                                                       Indels
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Y326_MYCGI
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleisechmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y326 MYCGE
P47568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYCGE
                                                                                                                                                                                                                                        LYMST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma genitalium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U39714; AAC71550.1; -. PIR; A64236; A64236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 33530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996
                                    Linacre A.,
Burke J.F.;
                                                 MEDLINE=90155411; Pulinacre A., Kellett
                                                                                                         Lymnaeoidea; Lymnaeidae; Lymnaea.
NCBI TaxID=6523;
                                                                                                                                     FMRFamide neuropeptides precursor.
Lymnaea stagnalis (Great pond snail).
Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                                                                                                                                                                     P19802;
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 2:
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15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2097;
related peptides are encoded
the snail Lymnaea stagnalis.
                        "Cardioactive neuropeptide Phe-Met-Arg-Phe-NH2
                                                                          TISSUE=Brain;
                                                                                                                                                                                                                               FMRF LYMST
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AMS; TIGRO0762; DegV; l.
hetical protein; Complete proteome.
NCE 295 AA; 33413 MW; 04610881C0F841EE CRC64;
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7; Conserv
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5 (Rel. 33, Last sequ
3 (Rel. 42, Last anno
al UPF0230 protein MG
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(Rel. 32, Last sequence update)
(Rel. 43, Last annotation update)
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                                                PubMed=1968092;
tt E., Saunders
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36.8%;
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                                                  Bright K.,
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Kelley J.M.,
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MBL outstation -
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Neuropeptide; Alternative systems, 1 35
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PROPEP 40 43
PROPEP 46 56
PROPEP 59 63
PROPEP 66 73
PROPEP 76 79
PREPTIDE 82 103
PROPEP 152 155
PROPEP 152 155
PROPEP 152 155
PROPEP 153 155
PROPEP 156 163
PREPTIDE 166 169
PREPTIDE 173 176
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                                                                                                                                                                                                                  EMBL; M37629; AAA63280.1; -.
EMBL; M67479; -; NOT ANNOTATI
EMBL; S38686; AAB21767.1; -.
EMBL; S34982; AAB21764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stagnalis: character:
peptide, 'SEEPLY'.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94108633; PubMed=7904219;
Santama N., Li K.W., Bright K.E.,
Benjamin P.R., Burke J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 82-103 (PN).
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                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              entities requires a license agreement
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                                                                                                                                                                        Amidation;
                                                                                                                                                                                               InterPro;
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Comment=Isoform
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ame=2; Synonyms=FMRFamide-related;
IsoId=P42565-1; Sequence=External;
                                                                                                                                                                                  Pro; IPR002544;
PF01581; FARP;
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IsoId=P19802-1; Sequence=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization and neuronal
                                                                                                                                                                     Cleavage on pair of basic residues; Repeat; Signal;
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llett E., Bright
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1 and isoform 2 only share the N-terminal signal
                                                                                                                                                           splicing
                                                             FLRF-AMIDE 2.
PN (SEEPLY).
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                                       FMRF-AMIDE
                                                                                                                       FLRF-AMIDE
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ng of an FMRFam:
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Q08874; Q08885; Q88203; Q08843; Q60781; Q60782;
Q951J72; Q9J1J3; Q9J1J4; Q9J1J5; Q9JIJ6; Q9JXX9;
16-QCT-2001 (Rel. 40, Created)
STRAIN=129/Sv; TISSUE-Heart;
MEDLINE=20253112; PubMed=10790403;
Hallsson J.H., Favor T
                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Microphthalmia-associated transcription factor.
MITF OR MI OR BW OR VIT.
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                                                                   MEDLINE=93345026; PubMed=8343963;
Hodgkinson C.A., Moore K.J., Nakayama A., Steingrimsson E.,
Copeland N.G., Jenkins N.A., Arnheiter H.;
"Mutations at the mouse microphthalmia locus are associated with
defects in a gene encoding a novel basic-helix-loop-helix-zipper
                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                  defects in a gene encoding
                                                                                                                 TISSUE=Melanocyte;
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                      Mus musculus (Mouse)
                                                 74:395-404(1993).
                                                                                                                                                                                                                                                                                            79
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                                                                                                                                                                                                                                                                                                                                          Similarity
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273
306 AA;
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273
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Pred. No.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                      AB2361EFF2C4EF18
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> Q (IN REF. 1)
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NN (G-64 PROVIDE AMIDE GROUP).
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        Lamoreux M.L.
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STRAIN=C57BL/6; TISSUB=Heart, and Melanocyte;
MEDLINE=95179171; PubMed=7874168;
Steingrimsson E., Moore K.J., Lamoreux M.L., Ferre-D'Amare A.R.,
Burley S.K., Sanders Zimring D.C., Skow L.C., Hodgkinson C.A.,
Arnheiter H., Copeland N.G., Jenkins N.A.;
"Molecular basis of mouse microphthalmia (mi) mutations helps explain
their developmental and phenotypic consequences.";
Nat. Genet. 8:256-263(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 345-392 FROM N.A.
STRAIN=C57BL/6; TISSUE=Heart;
MEDLINE=94012591; PubMed=8407885;
Hughes M.J., Lingrel J.B., Krakowsky J.M., Anderson K.P.;
"A helix-loop-helix transcription factor-like gene is located
"A helix-loop-helix transcription factor-like gene is located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics 155:291-300(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnusdottir R., Gunnarsson
Jenkins N.A., Steingrimsson
                                                                                                                                                                                                                                          Mol. Cell. Biol. 16:1203-1211(1996).

-I-FUNCTION: Transcription factor for tyrosinase and tyrosinase-
related protein 1. Binds to a symmetrical DNA sequence (E-boxes)

(5'-CACGTG-3') found in the tyrosinase promoter. Plays a critical 
role in the differentiation of various cell types as neural crest-
derived melanocytes, mast cells, osteoclasts and optic cup-derived 
retinal pigment epithelium.

-I-SUBUNIT: Efficient DNA binding requires dimerization with another 
bHLH protein. Binds DNA in the form of homodimer or heterodimer 
with either TPE3, TPEB or TPEC.

-I-SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "An LI element intronic insertion in the black-eyed gene: the loss of a single Mitf isoform responsible pigmentary defect and inner ear deafness.";
Hum. Mol. Genet. 8:1431-1441(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amae S., Fuse N., Yasumoto K.-I., Sato S., Yajima I., Yamamoto H., Udono T., Durlu Y.K., Tamai M., Takahashi K., Shibahara S.; "Identification of a novel isoform of microphthalmia-associated transcription factor that is enriched in retinal pigment epithelium."; Biochem. Biophys. Res. Commun. 247:710-715(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96182124; PubMed-8622664;
Takebayashi K., Chida K., Tsukamoto I., Morii B., Munakato
Arnheiter H., Kuroki T., Kitamura Y., Nomura S.;
"The recessive phenotype displayed by a dominant negative
microphthalmia-associated transcription factor mutant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yajima I., Sato S., Kimur
Goding C.R., Yamamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem.
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                                                                                                                                                                                                                                      ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99330550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT MI-BW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98321192;
                                                                                                                                                                                                                                                                                                                                                                                                                                     impaired nucleation potential.";
Mol. Cell. Biol. 16:1203-1211(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              locus."
                                                                                                                                                                                                                                  SUBCELLULAR LOCATION ALTERNATIVE PRODUCTS
                               Name=H1;
IsoId=Q08874-5; Sequence=VSP_002129, VSP_002132
                                                                                                                                                                                                                     Event=Alternative
                                                                         IsoId=Q08874-4;
                                                                                                            IsoId=Q08874-3;
                                                                                                                                              IsoId=Q08874-2; Sequence=VSP_002133;
                                                                                                                                                                                IsoId=Q08874-1; Sequence=Displayed;
   IsoId=Q08874-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem. 268:20687-20690(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gunnarsson G.J., eingrimsson E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10400990;
., Kimura T., Yasumoto K.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9647758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimura T.,
                                                                                                          Sequence=VSP_002131,
                                                                                                                                                                                                                     splicing; Named isoforms=9;
Sequence=VSP_002129, VSP_002132, VSP_002135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORMS H AND M),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sweet H.O., Copeland N.G.,
                                                                                                              VSP_002134,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND VARIANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Munakata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for the
                                                                                                                  VSP_002136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a result
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(MI-EW) HAS A NORMAL APPEARANCE AT THE HETEROZYGOUS STATE, BUT SHOWS WHITE COAT; EYES ALMOST ABSENT AND EYELLDS NEVER OPEN AT HOMOZYGOSITY, MICROPHTHALMIA-BLACK AND WHITE SPOT (MI-EWS) IS NORMAL AT HETEROZYGOSITY, AND PRESENTS WHITE SPOT SAND BLACK EYES AT HOMOZYGOUS STATE. MICROPHTHALMIA-WHITE (MI-WH) HAS REDUCED COAT COLOR AND EYE PIGMENTATION; SPOTS ON TOES, TAIL AND BELLY; INNER EAR DEFECTS AT HETEROZYGOSITY, AND AT HOMOZYGOSITY SHOWS WHITE COAT; EYES SMALL AND INNER IRIS SLIGHTLY PIGMENTED; SPINAL GANGLIA, ADRENAL MEDULLA AND DERMIS SMALLER THAN NORMAL, AND INNER EAR DEFECTS. MICROPHTHALMIA-VITILIGO (MI-VI) HAS NORMAL PHENOTYPE AT HETEROZYGOSITY, BUT SHOWS GRADUAL DEPIGMENTATION OF COAT, SKIN AND EYES, AND RETINAL DECENERATION AT HOMOZYGOSITY. HOWEVER, TYROSIMASE NORMAL PHENOTYPE; AT HOMOZYGOSITY, HOWEVER, TYROSIMASE NORMAL PHENOTYPE; AT HOMOZYGOSITY, HOWEVER, TYROSIMASE NORMAL PHENOTYPE; AT HOMOZYGOSITY, HOWEVER, TYROSIMASE ACTIVITY IN SKIN IS REDUCED. PIGMENTATION AT HOPESCTIVE IRISM (MI-DI) HAS REDUCED RETINAL DISMENTATION AT HOPESCTIVE IRISM SHOWS WHITE COAT; EYES OF REDUCED AND SHOWS WHITE COAT; EYES OF PROCESSION AND SHOWS WHITE COAT; EYES OF REDUCED AND SHOWS WHITE COAT; EYES OF REDUCED AND SHOWS WHITE COAT; EYES OF THE MOTOR SHOWS HOW THE COAT.
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DISEASE: DEFECTS IN MITF ARE THE CAUSE OF MICROPHTHALMIA (MI), A CONDITION CHARACTERIZED BY LOSS OF PICHENTATION; REDUCED EYE SIZE; FAILURE OF SECONDARY BONE RESORPTION; REDUCED NUMBERS OF MAST
                                                                                                                           REDUCED SIZED AND POSSIBLE MILD OSTBOPOROSIS AT HOMOZYGOSITY.

MICROPHTHALMIA-CLOUDY EYED (MI-CE) HAS A NORMAL APPEARANCE AT THE
HETEROZYGOUS STATE, BUT SHOWS WHITE COAT; EYES OF REDUCED SIZE AND
UNPICHENTED AT HOMOZYGOSITY. MICROPHTHALMIA-RED-EYED WHITE (MI-RW)
HAS A NORMAL APPEARANCE AT THE HOMOZYGOUS STATE, BUT SHOWS WHITE
COAT WITH ONE OR MORE PIGMENTED SPOTS AROUND THE HEAD/AND OR TAIL;
EYES ARE SMALL AND RED AT HETEROZYGOSITY. MICROPHTHALMIA-BLACK-
EYED WHITE (MI-BW) SHOWS A WHITE COAT BUT NORMAL SIZED EYES WHICH
REAMIN BLACK AT HOMOZYGOSITY.
SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=M1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q08874-8; Sequence=VSP_002130;
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AF222344; AAF63466
     AF222959;
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[9H223; Q9HAR1; Q9NZN2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
EH-domain containing protein 4 (EH domain-containing protein FKSG7)
[Hepatocellular carcinoma-associated protein 10/11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                 Wang Y.-G.;
"Cloning of FKSG7, a
                                                                                                                                Dong X. Y. Chen W.-F.; "Identification of genes which are differentially expressed hepatocellular carcinoma by SSH method."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       EHD4 OR FKSG7 OR HCA10 OR HCA11.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                       HUMAN
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                         "hEHD4, an EH domain containing protein-4.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                          Benjamin
                                                                              protein.";
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                   TISSUE=Hepatoma;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL :
                                                   SEQUENCE
                                                                     Submitted (SEP-2000)
                                                                                                                                                                                           NCBI_TaxID=9606;
SEQUENCE FROM N.A.
TISSUE=Brain, and Placenta
                                                                                                        FISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF222953
                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                          PAYSIPRKMGSNLEDILMD
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                                          Horowitz M.;
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                                                                                                                                                                                                              Chordata;
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                                                                                     novel gene which encodes
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RA Strausberg R.D., Cellins F.S., Wagner L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mass J.I., Wang J., Hsiah F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Wcorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wcorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
FI human and mouse cDNA sequences.",
FI proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20139435; PubMed=10673336; Pohl U., Smith J.S., Tachibana I., Ueki K., Lee H.K., Ramaswamy Pohl U., Smith J.S., Tachibana I., Ueki E.B., Louis D.N.; Wu Q., Mohrenweiser H.W., Jenkins R.B., Louis D.N.; "EHD2, EHD3, and EHD4 encode novel members of a highly conserved family of EH domain-containing proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932;
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CA BIND
CONFLICT
                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 EH domain.
-!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -|- TISSUE SPECIFICITY: Highly expressed in pancreas and --- SIMPLARITY: Contains 1 EH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
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                                                                                                                                                                                                                                                                                           PROSITE; PS00018; EF HAND; 1.
PROSITE; PS50031; EH; 1.
Calcium-binding; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_hc
                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 605892;
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AF181265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF454953;
BC006287;
 272
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 RLFEAEAQDLFRDI 285
                                    RAHDSEVQDLIRDI 21
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541 AA;
                                                                       Conservative
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57.1%;
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EF-HAND (POTENTIAL).
L -> I (IN REF. 2).
TEGPFNQGYGEGA -> PRAPSTRATGRVP
                                                                         Pred. No. 78;
?; Mismatches
                                                                                                           Score 41;
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                                                                                                                                                -> Q (IN REF. 2).
72DDE551829B7BF5 CRC64;
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                                                                                            78;
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                                                                                                           1,
                                                                                                           Length 541;
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA BOBAK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA BOBAK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Maddan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT human and mouse cDNA sequences."

"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

"Generation A.A. Sod. Sci. U.S.A. 99:16899-16903 (2002).

"C. -- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
-- C. -- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
Query Match
Best Local S
Matches 8
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Q9EQP2;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the ENropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by not be statement is not removed. Usage by an modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Czech II; TISSUE=Mammary gland; MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ICR;
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EMBL; BC007480; AAH07480.1; -.
MGD; MGI:1919619; 2210022F10Rik.
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15-MAR-2004 (Rel.
                                                                                                                                                Calcium-binding, ATP-binding.
NP BIND 68 75
DOMAIN 447 535
CA BIND 492 503
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InterPro; IPR000261; EPS15_homology.
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   Similarity
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541 AA;
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503 EF-HAND (POTENTIAL).
61480 MW; D34C28F046D740E1 CRC64;
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                                                                         DB 1;
                                                                      Length 541;
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Qy 8 RAHDSEVQDLIRDI 21
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Db 272 RLFEABAQDLFRDI 285

Search completed: May 4, 2004, 09:10:38
Job time: 11 secs

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Copyright (c) 1993 - 2004 Compugen Ltd
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    Q7XPP0
Q7XXP3
Q85782
Q851800
Q81800
Q7XFS6
Q7XXE8
Q7XXE8
Q7XXP5
Q7XXP5
Q7XXP7
Q7XFP8
Q818A6
Q816A6
Q816A6
                                                                                                            Q7XM7C
   Qenyj homo sapien
Qenyj homo sapien
Qenyj homo sapien
Qenyj homo sapien
Qenyj sativ
Qenyj sativ
Qenyj oryza sativ
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                                                                                                                                                                                                                                                                     O9h769 homo sapien Q95wu6 giardia lam Q8gm65 bifidobacte Q9ns15 homo sapien Q8gpy3 influenza a Q7xm07 oryza sativ Q8fuh3 corynebacte Q7xxi5 oryza sativ Q20710 caenorhabdi Q9nvj7 homo sapien Q9vv74 homo sapien
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borrelia bu
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Q59983 ID Q599 AC Q599 AC Q599 AC Q599 DT 01-N DT 01-J DNA Seq. 4:19-27(LJJ).

EMBL; D13858; BAA02976.1; -.

EMBL; D13858; BAA02976.1; -.

EMBL; D13858; BAA02976.1; -.

GO; GO:0016757; F:transferase activity, transferring glycosyl.

R GO; GO:0016757; F:glucan biosynthesis; IEA.

R GO; GO:001250; P:glucan biosynthesis; IEA.

R InterPro; IPR002479; CW_binding.

R InterPro; IPR00318; Glyco_hydro_70.

R Ffam; PF01473; CW_binding_1; 13.

DR Pfam; PF01324; Glyco_hydro_70; 1.

CHATN

Glycosyltransferase; Signal; Transferase.

ET GLYCOSYLTRANSFERASE-I.

GLUCOSYLTRANSFERASE-I.

GLUCOSYLTRANSFERASE-I.

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                    GLUCOSYLTRANSFERASE.
Streptococcus sobrinus.
Bacteria, Firmicutes, La
Streptococcus.
NCBI_TaxID=1310;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5).
GTFI.
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                                                                                                                                                                                                                  Q55263;
Q55263;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato S., Inoue M., Handa N., Aizawa Y., Isobe "DNA sequence of the glucosyltransferase gene Streptococcus sobrinus.";
DNA Seq. 4.19-27(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus sobrinus
                                                                                                                                                 GTF-I.
                                                                                                                                                                     01-JAN-1998
01-JUN-2003
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                                                                             Lactobacillales;
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Q7XX75
Q7XWL9
Q7XSB6
Q9AYB5
Q7X978
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Q9C0A3
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Q83ZD6
Q7XIAO
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Last sequence task anno
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Pred. No. 3.6e-08;
1; Mismatches 0;
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annotation
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Q9y3s1 h
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Q7xx75
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1 homo sapien
6 staphylococ
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Q46756
ID Q4671
AC Q487
DT 01-N
DT 01-N
DT 01-N
DT 01-N
DT 01-O
DD Dext
COC Bact
OC WCECT
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Q84CN4
ID Q8
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Best Local Similarity
Matches 21; Conserv
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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PIR; JC5473; JC5473.

GO; GO:0009250; P:glucan biosynthesis; IE

GO; GO:0009250; P:glucan biosynthesis; IE

InterPro; IPR002219; CW binding.

InterPro; IPR003318; Glyco hydro 70.

Pfam; PF02324; Glyco hydro 70; 1.

SEQUENCE 1290 AA; 145590 MW; 3555C2E5
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Q48756;
01-NOV-1996
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Q84CN4;
01-JUN-2003
01-JUN-2003
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJINE 97136686; PubMed=8982063;
MEDIJINE 97136686; PubMed=8982063;
Monchois V., Willemot R.M., Remaud-Simeon M., Croux C., Monsan P.;
"Cloning and sequencing of a gene coding for a novel dextransucrase from Leuconostoc mesenteroides NRRL B-1299 synthesizing only alpha (6) and alpha (1-3) linkages.";
Gene 182:23-32(1996).
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                    Bacteria;
                                                                 DSRR
                                                                                       Dextransucrase
                                          Leuconostoc
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                      Firmicutes;
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                                          mesenteroides
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
ise DSTR (EC 2.4.1.5).
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95.5%;
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76.2%;
                      Lactobacillales; Leuconostoc
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Pred. No. 3.6e-08;
1; Mismatches 0
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Last annotation updat
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RESULT
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Best Local S
Matches 15
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

REMBL, Au250172; CAB76555.1; --
REGO; GO:0016757; F:transferase activity, transferring glycos
REGO; GO:009250; F:glucan biosynthesis; IEA.

REGO; GO:000279; CM binding.

REINTERPRO; IPR003318; Glyco_hydro_70.

REINTERPRO; IPR003318; Glyco_hydro_70; 1.

REPfam; PF01473; CM binding 1; 13.

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Best Local Similarity
Matches 15; Conserv
Q9EZH5;
Q9EZH5;
01-MAR-2001
01-MAR-2001
01-JUN-2003
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Q9L466;
01-OCT-2000
01-OCT-2000
01-JUN-2003
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"Gene encoding a dextransucrase
NRRL B-1501.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 7
Pfam; PF01473; CW binding 1; 11.
Pfam; PF02324; Glyco hydro 70; 1.
Glycosyltransferase; Transferase.
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GO; GO:0002250; P:glucan biosynthesis; IEA.
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Bacteria; Firmicutes; Lactobacillales; Leuconostoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willemot R.M., Monsan P.; 
"Sequence analysis of the gene encoding alternansucrase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1245;
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  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                    PRELIMINARY;
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68.2%;
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Pred. No. 0.00
3; Mismatches
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01-JUN-1998
01-JUN-2003
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"Leuconostoc mensenteroides B-742CB, a dextransucrase gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF294469; AAG38021.1;
EMBL; AF294469; P.glucan biosynthesis; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF0473; CW binding_1; 13.
Pfam; PF03224; Glyco hydro 70; 1.
SEQUENCE 1508 AA; 168542 MW; E2FCFA0F87AE4F3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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IPNYSFVRAHDSEVQTVIAQII 655
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68.2%;
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(TrEMBLrel. 15,

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PRELIMINARY;

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P SEQUENCE FROM N.A.

RT SINGH D.K.S.;

AB Bhatnagar R., Singh D.K.S.;

RT Cloning and Molecular Characterization of Dextransucrase General Content of of Dextransucrase General Co
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DT 01-V
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Q9ZAR4;
01-MAY-1999
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STRAIN-NRRL B-512F;
MEDLINE-20169623; PubMed-10705445;
Funane K., Mizuno K., Takahara H., Kobayashi
"Gene encoding a dextransucrase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P06278; 1VJS.
HSSP; P06278; P:glucan biosynthesis;
GO; GO:0009250; P:glucan biosynthesis;
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF02324; Glyco hydro 70; 1.
SEQUENCE 1016 AA; 110344 MW; 8896E
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01-0CT-2003
Q8KRE1;
Q8KRE1;
01-OCT-2002
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Biosci. Biotechnol. Biochem. 64:29-38(2000)
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01-MAY-1999 (TrEMBLrel. 10,
01-OCT-2003 (TrEMBLrel. 25,
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Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RMBL; ANO17384; AAGG1158.1;-
RGO; GO:0016757; F:transferase activity, transferring glycos;
RGO; GO:0009250; P:glucan biosynthesis; IEA.
RInterPro; IPR002479; CM binding.
RInterPro; IPR002479; CM binding.
R InterPro; IPR003318; Glyco.hydro_7:
R Pfam; PF01473; CM binding.
R Pfam; PF02324; Glyco.hydro_7; 1.
R Pfam; PF02324; Glyco.hydro_7; 1.
R Transferase; Glycosyltransferase.
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009250; P:glucan biosynthesis; IEA.
InterPro; IPR002479; CW binding.
InterPro; IPR00318; Glyco_hydro_70.
Pfam; PF01473; CW binding 1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
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MEDLINE=21958684; PubMed=11960691;
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Matches 14; Conserv
                                                                                                                                                                                 MEDLINE-2231661; PubMed=12270834; MEDLINE-2231661; PubMed=12270834; Bozonnet S., Dols-Lafargue M., Fabre E., P Mondan P., Willemot R.M.;

Molecular characterisation of DSR-E, an a synthesising dextransucrase with two catal J. Bacteriol. 184:5753-5761(2002).

EMBL; Au430204; CAD22883.1; -.

EMBL; Au430204; CAD22883.1; -.

GO; GO:0016757; F:transferase activity, tr GO; GO:0016757; F:transferase activity. Transferase; IPR002479; CW binding.

InterPro; IPR003318; Glyco hydro_70.

Pfam; PF01473; CW binding 1; 20.

Pfam; PF02324; Glyco hydro_70; 2.

Transferase; Glycosyltransferase.

NON "WEO"
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01-NOV-1999
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8G9Q2
Q8G9Q2;
01-MAR-2003
01-MAR-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0046821; C:extrachromosomat was, GO; GO:00950; P:glucan biosynthesis; InterPro; IPR003479; CW binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW binding_1; 11.
Pfam; PF02324; Glyco_hydro_70; 1.
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"S.cricetus glucosyltransferase(gtfS and gtfT)
"S.cricetus glucosyltransferase(gtfS and gtfT)
submitted (MAR-1999) to the EMBL/GenBank/DDBJ c
EMBL; AB026123; BAA77237.1; -.
EMBL; AB026123; BAA77237.1; -.
EGO; GO:0046821; C:extrachromosomal DNA; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pAM1
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01-MAR-2003 (TrEMBLrel. 23,
01-JUN-2003 (TrEMBLrel. 24,
Dextransucrase (EC 2.4.1.5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Lactobacillales; Leuconostoc
NCBI_TaxID=1245;
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          Conservative
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                                                                                                                              313264 MW; D03262CDD735399D CRC64;
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Last sequence
Last annotation
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   Score 73; DB 2;
Pred. No. 0.028;
3; Mismatches
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Last annotation update)
(Fragment).
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Pred. No.
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catalytic domains.";
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                                                                    Length 2835;
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RESULT
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Best Local S
Matches 15
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"S.cricetus glucosyltransferase(gtfs and gtfT) ge
"S.cricetus glucosyltransferase(gtfs and gtfT) ge
submitted (MRR-1999) to the EMBL/GenBank/DDBJ dat
EMBL, AB026123; BAA77236.1; -.

GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0009250; P:glucan biosynthesis; IEA.
InterPro; IPR002479; CW binding.
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01473; CW binding 1; 9.
Pfam; PF01473; CW binding 1; 9.
encoding glucosyltransferase from Streptococcus or:
Infect. Immun. 68:2475-2483 (2000).

ENBL; AB025228; BAA95201.1; ...
EQO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009250; F:glucan biosynthesis; IEA.
InterPro; IPR002479; CW binding.
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro_70.
Pfam; PF01473; CW binding_1; 16.
Pfam; PF02324; Glyco hydro_70; 1.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Glucosyltransferase.
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Q9WXJ4;
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01-JUN-2003
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                                                                                                                                                                                                                       STRAIN=ATCC10557;
MEDLINE=20231779; PubMed=10768934;
MEDLINE=20231779; PubMed=10768934;
Fujiwara T., Hoshino T., Ooshima T., Sobue S., Hamada S.
"Purification, characterization, and molecular analysis"
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
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) (TrEMBLrel. 12,
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24,
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Last sequence update)
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Pred. No. 0.03
1; Mismatches
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0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcaceae;
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                                                                                                                                                                                                                                                          Hamada S.;
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RESULT 17

Q00599

ID Q0059

AC Q0059

DT 01-NC

DT 01-NC

DT 01-NC

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DT 01-CC

DE Gluck

GN GTFK
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Q54178
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Best Local S
Matches 14
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Best I
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Q00599 PREFIG. 01, Created)
Q10599;
Q1 NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1 NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1 OCT-2003 (TrEMBLrel. 25, Last amotation update)
Glucosyltransferase S precursor (EC 2.4.1.5) (GTF)
(Sucrose 6-glucosyltransferase).
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Q54178; Q542
Q5-NOV-1996
Q1-NOV-1996
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92276337; PubMed=1534326;
Sulavik M.C., Tardif G., Clewell
"Identification of a gene, rgg, w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96157084; PubMed=8586195; Vickerman M.M., Sulavik M.C., Clewell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcue.
NCBI_TaxID=293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus gordonii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016740; F:transferase activity;
GO; GO:0009250; F:glucan biosynthesis;
InterPro; IPR0032479; CW binding:
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01473; CW binding I; 13.
Pfam; PF02324; Glyco hydro 70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 174:3577-3586(1992)
EMBL; U12643; AAC43483.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular analysis of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gordonii Challis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B41898; B41898.
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                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      177805 MW;
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Last
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Pred. No. 0.045;
2; Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      5AE0328DC5E08D18 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spp phenotype
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RESULT 18
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Best Local :
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Giffard P.M., Simpson C.L., Milward C.P., Jacques N.A.;
Giffard P.M., Simpson C.L., Milward C.P., Jacques N.A.;
Molecular characterization of a cluster of at least two
"Molecular characterization of streptococcus salivarius ATCC 25975.";
J. Gen. Microbiol. 137:2577-2593(1991).

-i. FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
-play A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
THEIR ABILITY TO ADHERE TO SMOOTH SUFFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS
-i. CATALYTIC ACTIVITY: SUCROSE + (1,6)-ALPHA-D-GLUCOSYL)(N) = D-
FRUCTOSE + (1,6)-ALPHA-D-GLUCOSYL)(N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giffard P.M., Allen D.M., Milward C.P., Simpson C.L., Jacques "Sequence of the gtfK gene of Streptococcus salivarius ATCC 25 evolution of the gtf genes of oral streptococci."; J. Gen. Microbiol. 139:1511-1522(1993).
                                                                                                                                                      01-AUG-1998
01-AUG-1998
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPHA ANYLASES AND RABBIT GLYCOGEN PHOSPHORYLASE.
EMBL; Z11872; CAA77898.1; -.
EMBL; Z11873; CAA77901.1; -.
EMBL; M64111; AAA26897.1; -.
PIR; S22737; S22737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=ATCC 25975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                           068542;
                                                                                                                                                                                                                                                                                                                                                                                                                 QO; GO:0016757; P:transferase activity, tr
GO; GO:0009250; P:glucan blosynthesis; IEA
InterPro; IPR002479; CW binding.
InterPro; IPR002318; Glyco hydro_70.
Pfam; PF01473; CW binding 1; 13.
Pfam; PF02324; Glyco hydro_70; 1.
Transferase; Glycosyltransferase; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
-1- DISEASE: DENTAL CARIES.
-1- SIMILARITY: TO REGIONS OF BARLEY AND BACILLUS AMYLOLIQUEFACIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93381463;
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                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                        Glucosyltransferase
"Streptococcus
Submitted (FEB
                                                                     NCBI_TaxID=1304;
                                                                                                                Streptococcus salivarius.
                         Jaffe R.I.;
                                      STRAIN=V1477;
                                                  SEQUENCE FROM N.A.
                                                                                      Streptococcus
                                                                                                   Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                          l Similarity
14; Conserv
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  occus salivarius V1477
(FEB-1998) to the EMBI
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                                                                                                                                                       (TrEMBLiel.) (TrEMBLiel.) (TremBLiel.)
                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                     Lactobacillales;
                                                                                                                                            (Fragment)
                                                                                                                                                       24,
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                                                                                                                                                      Last sequence update)
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    L477 gtfN.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                         Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
GLUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                           593
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                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transferring IEA.
                                                                                                      Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Dental caries
     databases
                                                                                                                                                                                                                                                                                                                                                        Length 1599
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RESULT 19
055264

10 05526

AC 05526

DT 01-N(
DT NC)
RC NCER
RN N
  RESULT 20
Q9RE05
ID Q9RE0
AC Q9RE0
DT 01-MA
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PIR; T30552; T30552;
GO; GO:0016740; F:transferase activity; IE:
GO; GO:0016740; F:transferase activity; IE:
GO; GO:0009250; P:glucan biosynthesis; IEA
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 70.

Pfam; PF01473; CW binding I; 7.

Pfam; PF01473; CW binding T; 7.
                                                                                                           Q9RE05;
Q9RE05;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q55264; PRELIMINARY; Q55264; 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding for primer-independent glucosyltransferases."; Infect. Immun. 63:609-621(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95122197; PubMed=7822030;
Simpson C.L., Giffard P.M., Jacques N.A.;
"Streptococcus salivarius ATCC 25975 poss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus salivarius.
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                                                                   01-MAR-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                              Alternansucrase
Leuconostoc mesenteroides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
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GO:0009250; P:glucan biosynthesis; IEA.
erPro; IPR002479; CW_binding.
erPro; IPR003318; Glyco hydro_70.
m; PF01473; CW_binding_1; 7.
m; PF02324; Glyco_hydro_70; 1.
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1449 AA;
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                                              (TrEMBirel. 13, Created)
(TrEMBirel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation updat
(ase (EC 2.4.1.140).
                                                                                                                                                            PRELIMINARY;
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65.0%;
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                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                      RC STRAIN=ATCC 25975;

RM MEDLINE=92140377; PubMed=1838391;

RA MEDLINE=92140377; PubMed=1838391;

RA Giffard P.M.; Simpson C.L., Milward C.P., Jacques N.A.;

RA Giffard P.M.; Simpson C.L., Milward C.P., Jacques N.A.;

RY "Molecular characterization of a cluster of at least two

"Molecular characterization of a cluster of at least two

"Molecular characterization of a cluster of at least two

"Molecular characterization of a cluster of at least two

"Molecular characterization of the play a REC 25975.";

RI . Gen. Microbiol. 137:2577-2593(1991).

"I . Gen. Microbiol. 137:2577-2
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EMBL, AJ250173; CAB65910.2; -.

GO; GO:0016757; F:transferase activity, tr
GO; GO:0009250; P:glucan biosynthesis; IEA
InterPro; IPR002479; CW binding
InterPro; IPR00318; Glyco hydro_70.

Pfam; PF01473; CW_binding_T; 11.

Pfam; PF01473; CW_binding_T; 11.

Pfam; PF02324; Glyco_hydro_70; 1.

Glycosyltransferase; Transferase.

SEQUENCE 2057 AA; 228987 MM; 62BCE9385
PIR; A44811; A44811.

PIR; A44811; A44811.

GO; GO:0016757; F:transferase activity, transfer GO; GO:009250; P:glucan biosynthesis; IEA.

InterPro; IPR002479; CW binding.

InterPro; IPR003318; Glyco hydro 70.

Pfam; PF01473; CW binding_1; 11.

Pfam; PF02324; Glyco hydro 70; 1.

Pfam; PF02324; Glyco hydro 70; 1.

Transferase; Glycosyltransferase; Repeat; Dental DOMAIN 1307 1388 6 DIRECT REPEATS.

REPEAT 1307 1338 PEPEAT 2.
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Q00600;
01-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Glucosyltransferase I (EC 2.4.1.5) (GTF) (Dextransucrase)
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STRAIN=NRRL B-1355;
MEDLINE=20080809; P
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Willemot R.M., MonBan P.
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12; Conser
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63.2%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B-1355.";
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Q9ZIX9
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Best Local 9
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Matches 12
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                                                                                                                                                                                                                                                                        GO; GO:0016740; F:transferase activity; IE
GO; GO:0009250; P:glucan biosynthesis; IEA
InterPro; IPR004829; Csurface antigen.
InterPro; IPR002479; CW_binding.
InterPro; IPR00318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF03224; Glyco_hydro_70; 1.
Probom; PD153422; Csurface_antigen; 1.
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Q55265;
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01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  Simpson C.L., Giffard P.M., Jacques N.A.; "Streptococcus salivarius ATCC 25975 possesses at least coding for primer independent glucosyltransferases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus salivarius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucosyltransferase precursor.
                                                                                                                                                                                                                                                          Signal; Transferase.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                 EMBL; L35928; AAC41413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=95122197; PubMed=7822030;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                     Hypothetical protein (Fragment).
Borrelia burgdorferi (Lyme disease spirochete)
Bacteria; Spirochaetes; Spirochaetales; Spiroc
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Infect.
 STRAIN=N40;
          SEQUENCE FROM N.A.
                           NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                         T30858; T30858.
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12; Conserv
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1577 AA;
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                                                                  (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
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                                                                  10, Created)
10, Last sequence update)
25, Last annotation update)
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PEPEAT 5.
PEPEAT 6.
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Pred. No. 0.86
4; Mismatches
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GLUCOSYLTRANSFERASE.
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Best Local S
Matches 10
                                                                                                                                                                                                                                                    Lengeler K.B., Fox D.S., Fraser J.A.
Dietrich F.S., Heitman J.;
Submitted (SEP-2002) to the EMBL/Ge:
EMBL; AF542529; AAN75169.1; -.
GO; GO:0016459; C:myosin; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; I
InterPro; IPR001609; myosin_head Pfam; PP01843; DIL; 1.
Pfam; PP00612; 1Q; 6.
Pfam; PP00612; TQ; 6.
Pfam; PP00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1
SMART; SM00015; TQ; 6.
SMART; SM00242; MYSC; 1.
SEQUENCE 1554 AA; 174915 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8J0Z6;
01-MAR-2003
01-MAR-2003
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF006036; AAD01254.1; -.
Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang P., I
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE=20570501; PubMed=11121047; Lengeler K.B., Wang P., Cox G.M., Perfect J.R., Heitman J.; "Identification of the MATA mating-type locus of Cryptococcus neoformans reveals a serotype A MATA strain thought to have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lengeler K.B., Fox D.S., Fraser J.A., Dietrich F.S., Heitman J.;
"Mating-type locus of Cryptococcus neof sex chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 940-1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=178876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22343086; PubMed=12455690;
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                                                                                                                                                                                     InterPro; IPR002710; DIL.
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryot. Cell 1:704-718(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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1 (JAN-2002)
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(TrEMBLrel.
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         174915 MW;
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Last annotation update)
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Pred. No.
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pfam; pe01843; DIL; 1.
pfam; pe00612; IQ; 6.
pfam; pe00613; myosin_head; 1.
prINTS; pr000135; myosin_head; 1.
prIDOm; pD0001355; myosin_head; 1.
swart; sw00015; IQ; 6.
swart; sw000142; mysc; 1.
swart; sw000242; mysc; 1.
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"Mating-type locus of Cryptococcus neofo of sex chromosomes.";
Eukaryot. Cell 1:704-718(2002).
Eukaryot. Cell 1:704-718 (2002).
EMBL; AF545531; AAN75723.1; --
GO; GO:0016459; C:myosin; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
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Q8J0W2;
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P74028;
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InterPro; IPR00048; IQ_region.
InterPro; IPR001609; myosin_head.
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Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
               MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S.
Hosouchi T., Matsuno A., Muraki A., Nakazaki N.,
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                                                                                                     SEQUENCE FROM N.A.
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RP STRAIN-VPI-5482 / ATCC 29148;

RX MEDLINE=2255085; PubMed=12663928;

RX MID. Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

RC Chiang H.C., Hooper L.V., Bacteroides thetaiotaomicron symbiosis.";

RT Science 299:2074-2076(2003).

REMEL; ABO16939; AA078223.1; -.

RO; GO:000066; F:acyl carrier activity; IEA.

RO; GO:000663; F:acyl carrier activity; IEA.

RO; GO:000663; P:pyrimidine base metabolism; IEA.

RO; GO:0006206; P:pyrimidine base metabolism; IEA.

RO; GO:0006206; P:pyrimidine base metabolism; IEA.

RO; GO:0006231; Acyl carrier.

RI InterPro; IPR003231; Acyl carrier.

RR FFODOM; PR003281; Acyl carrier; 1.

RFCDDOM; PR003710; ApbA; 1.

RFCDDOM; PR000887; Acyl carrier; 1.
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EMBL, D90911, BAA18101.1; -.

PIR; S75540; S75540.

EYPOTHETISTS 375540; S75540.
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MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
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STRAIN-Classical 569B / ATCC 25870 / Serotype Ol; TRANSP Clark C.A., Manning P.A.;
"The Vibrio cholera Mega-integron.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q983M9;
01-OCT-2001
01-OCT-2001
01-JUN-2003
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SEQUENCE 5
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EMBL; AE004379; AAF96375.1;
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Vibrionaceae; Vibrio.
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DNA Res. 7:331-338(2000).

EMBL; AP003013; BAB53851.1; -...
GO; GO:0004222; F:metalloendopeptidase activity;
GO; GO:0004222; P:proteolysis and peptidolysis;
InterPro; IPR001431; Peptidase M16.
InterPro; IPR001431; Peptidase M16.
Pfam; PP00575; Peptidase M16; 1.
Pfam; PP05193; Peptidase M16; 1.
                                                                                                                                                                                                                                                MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishawa C., Kohara M., Matsumoto M., Matsuno A., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                   "Complete genome structure of the nitrogen-fixing Mesorhizobium loti.";
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51 AA; 5824
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EMBL; AB003108; AAF30492.1; -.

GO; GO:0005663; C:DNA replication factor of the control of the cont
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SEQUENCE
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Cassell G.H.;
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Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; U
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SMART; SM00382; AAA;
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Result No.

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RESULT 1
US-09-210-361-4
PRIOR APPLICATION NUMBER: 01.16
PRIOR FILING DATE: 1998-01.16
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
LENGTH: 1375
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CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-09,620
EARLIER FILING DATE: 1998-01-20
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR PELICATION NUMBER: 09/007,999
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/478,704
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR APPLICATION NUMBER: 09/008,172
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20; Conservative
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SEQ ID NO 4
LENGTH: 1375
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Patent No. 6465203
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
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TITLE OF INVENTION: Substitutes for Modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions and Paper
FILE REFERENCE: 0357CRD
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o. 6284479
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                                                                                    FastSEQ for Windows Version 3.0
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90.9%; Pred. No. 3
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; ORGANISM: streptococcus mutans US-09-740-274-4
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US-09-007-999-2
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; TYPE: PRT ; ORGANISM: Streptococcus mutans US-09-210-361-2
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APPLICANT: Nichols, Scott B.
TITLE OF INVENTION: Substitutes for Modified Starch
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0356D
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Patent No. 6087559
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SEQ ID NO 2
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CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
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NUMBER OF SEQ ID NOS: 2
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EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
                                                                                                                                          NUMBER OF SEQ ID NOS:
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-01-16
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tent No. 6284479
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Pred. No. 5.4e-08;
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RESULT 5
US-09-740-274-2
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US-09-740-274-2
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PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/009,620
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TYPE: PRT
ORGANISM: Leuconostoc mesenteroides
-09-604-957-5
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CURRENT FILING DATE: 2000-12-19
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TITLE OF INVENTION:
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APPLICANT: DIJKHUIZEN, LUBBER
APPLICANT: RAHAOUI, HAKIM
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PRIOR APPLICATION NUMBER: 08/482,711
PRIOR FILING DATE: 1995-06-07
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                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
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                                                                SOFTWARE:
                                                                                                            PRIOR APPLICATION NUMBER: 00201871.1 PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
                                                                                                  NUMBER OF SEQ ID NOS: 17
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                                             LENGTH: 523
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similarity 90.9%;
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Pred. No. 5.4e-08;
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US-09-604-957-7
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CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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Best Local Similarity
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                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
SOPTWARE: PATENTIN VET. 2.1
SEQ ID NO 3
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Best Local Similarity
                                                                   Matches
                                                                                                Query Match
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APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
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                                                                                                                                                                    LENGTH: 12
TYPE: PRT
                                                                                                                                                      ORGANISM: Lactobacillus reuteri
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 620 IPNYSEVRAHDNNSQDQIQNAI 641
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                          1 VPSYSFARAHDSEVQDLIRDII 22
                                                                   | Similarity
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                                                                  61.8%; Score 68; DB 4; larity 54.5%; Pred. No. 0.0077; Conservative 5; Mismatches
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63.6%;
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Pred. No. 3.7e-05;
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Pred. No.
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US-09-499-203-2
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US-09-604-957-6
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; ORGANISM: Leuconostoc mesenteroides
US-09-604-957-6
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APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: RESER, ROBERT-UAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: E0 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
CURRENT FILING DATE: 2000-06-28
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               GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
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Matches
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SEQ ID NO 6
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APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
FILE REPERENCE: 147-1969
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
                                                                                                    Sequence 4, Application US/09604957 Patent No. 6486314
                                                                                                                                                                                                                                                                                                                           Query Match
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PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
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ORGANISM: Leuconostoc mesenteroides
TITLE OF INVENTION:
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Local Similarity 63.2%;
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NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
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Pred. No.
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Pred. No. 0.021;
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; LENGTH: 545
; TYPB: PRT
; ORGANISM: Streptococcus mutans
US-09-604-957-4
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US-09-008-172-2
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US-09-210-361-6
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SOFTWARE: PatentIn Ver.
SEQ ID NO 4
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Patent No. 6127602
CENERAL INFORMATION:
                                 CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER FILING DATE: 1998-01-20
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LENGTH: 14
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILLING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09210361
Patent No. 6284479
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EARLIER
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FILING DATE:
                    FILING DATE: 1995-06-07
APPLICATION NUMBER: 09/008,172
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65.0%;
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Pred. No. 0.028;
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Pred. No. 0.
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ORGANISM: streptococcus mutans
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US-08-793-824-2
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LENGTH: 1430
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Best Local S
Matches 13
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Patent No. 64652
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Best Local Similarity 65.0%;
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EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1430
TYPE: PRT
ORGANISM: streptococcus mutans
-09-740-274-6
                                                                                                                                                        Patent No.
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PRIOR FILING DATE: 1998-C
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1995-C
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
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TITLE OF INVENTION: Glucan-c
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PRIOR APPLICATION NUMBER: 08/482,711
PRIOR FILING DATE: 1995-06-07
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                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                             APPLICANT: Simpson, Christine Lynn
APPLICANT: Giffard, Philip Morrison
APPLICANT: Jacques, Nicholas Anthony
TITLE OF INVENTION: Genetic Manipulation of Plants to
TITLE OF INVENTION: Increase Stored Carbohydrates
NUMBER OF SEQUENCES: 2
                  CORRESPONDENCE ADDRESS:
 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/
FILING DATE: 1995-06-07
APPLICATION NUMBER: 09/
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                                                                                                                                                                                                                                                                                                                               l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 3.0
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                                                                                                                                                                     Application US/08793824
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Griffith Hack & Co
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; Pred. No. 0.09
2; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1577 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION UMBER: AU PM7643
PILING DATB: 24-AUG-1994
PELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 957 5944
TELEPAX: 61 2 957 6288
TELEPAX: 6547
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5919656el Genes Encoding Telomerase
TITLE OF INVENTION: 1
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ORIGINAL SOURCE:
ORGANISM: Stre
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,189
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
                                                ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                            ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
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                                                                                                                                                                                                                                                             ZIP: 91320-1789
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No. 5981838th Sydney
New South Wales
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                                                     34,688
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Pred. No. 0.1;
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                                                      RESULT 18
US-09-184-445-3
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Best Local
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                      Patent No. 6174703
                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFO
                                                                                                                                                                                                                                                                                                                                   NAME: Oleski, Nancy A. REGISTRATION NUMBER: 34,65 REFERENCE/DOCKET NUMBER: FINFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1010 - CITY: Thousand Oaks
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/751,189 FILING DATE: 15-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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LENGTH: 2627 amino acids
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les 8; Conserv
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STRANDEDNESS: un
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TOPOLOGY: unl
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                                                                                                                                                                                     Local
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                                                                                                                  205 MPSYSLSLGEEEEVEDL 221
             INFORMATION:
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                                                                                                                                            1 VPSYSFARAHDSEVQDL 17
                                                                                                                                                                    Similarity 47.1%;
8; Conservation
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                                                                                                                                                                                                                                                                                          amino acid
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                                         Application US/09184445
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1840 De Havilland Drive
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ilarity 47.1%;
Conservative
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Harrington, Lea A.
                                                                                                                                                                                                                                                              unknown
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    Murray O.
    No. 5981707el Genes Encoding Telomerase Protein

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                                                                                                                                                                         Score 45; DB 2; Lei
Pred. No. 1.4e+02;
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1990-08-13
PERIOR APPLICATION NUMBER: US 60/064,964
PRIOR RILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4115
LENGTH: 501
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                                                                                                                                ORGANISM: Staphylococcus epidermidis US-09-134-001C-4115
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ATTORNEY/AGENT INFORMATION:
NAME: Oleek!, Nancy A.
REGISTRATION NUMBER: 34.688
REFERENCE/DOCKET NUMBER: A-43:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 4115, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: LYNn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                         Matches
                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERAFING SYSTEM: PC-DOS/MS-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,445
APPLICATION NUMBER: US/09/184,445
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LENGTH: 2627 amino acids
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity les 8; Conserv
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1 VPSYSFARA---HDSEVQDLIR 19
                                                           10;
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ilarity 47.1%;
Conservative 4
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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                                                                            45.5%;
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Pred. No.
                                                           5; Mismatches
                                                                            Score 44.5;
Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4e+02;
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                                                                                                   DB 4;
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                                                                                                 Length 501;
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US-09-345-473E-37
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TITLE OF INVENTION: No. 6558903el Kinases and Uses
FILE REFERENCE: 35000/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08913578
Patent No. 6218159
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Best Local Similarity
                                                                                                                                                           FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 9601069.9
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION UMBER: 98.891
REFERENCE/DOCKET NUMBER: 931352
TELECOMMUNICATION IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hodgson, APPLICANT: Lawlor, I
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                             TYPE: amino acid
                                                                                                                                 TELEFAX:
                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/913,578
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                               STRANDEDNESS: single
                 COPOLOGY:
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                                                                  484 amino acids
                                                                                                                                 610-270-4478
610-270-5090
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 peptide
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US-08-785-427-2
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                                                                                               US-08-557-309B-37
                                                                                                               RESULT 23
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,427
                                                                 Patent No.
                                                                               Sequence 37, Application US/08557309B
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6238900el trna synthetase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 9601069.9
APPLICATION NUMBER: 9601069.9
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKST NUMBER: P313
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                GENERAL INFORMATION:
APPLICANT: Reed, S'
APPLICANT: Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acid
 APPLICANT:
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Local Similarity 40.9%;
hes 9; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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Reed, Steven G.
Skeiky, Yasir A.W.
Lodes, Michael J.
                                                                                                                                                                                                                            Conservative
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)9 Swedeland Road
                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                           39.5%;
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Pred. No. 32;
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Pred. No. 3
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US-08-557-309B-37
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.422
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/08834306 Patent No. 6054135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Reed, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 639 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Seattle
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                   CITY: Seattle
                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION:
                                                 CLASSIFICATION:
                                                                                                                                                                                                   ZIP: 98104-7092
                                                                                                                                                                                                                                                                     STREET:
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 VPGWSEALLHDAEFQQL 495
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                                                                                                                                                                                                                                                                      6300 Columbia Center,
                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                       Steven G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             701 Fifth Avenue
                                                                                                                                                                                                                                                                        701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 639
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                                                                                             Matches
                             479 VPGWSEALLHDAEFQQL 495
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US-08-834-306-37
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 639 anino acids
                                                                                           TOPOLOGY:
US-08-993-674A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Apparent No. 6228
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.427
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                              Query Match
Best Local (
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
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                                                                                                                           TYPE: amino
                          Local Similarity
les 9; Conserva
                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                           ENGTH:
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amino acid
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VPSYSFARAHDSEVODL 17
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VENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
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Lodes, Michael J.
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                                                                                                                                                                                                       (206) 622-4900
(206) 682-603
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                                 Conservative
                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yasir A.W.
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Pred. No. 55;
                                                   Score 43; DB
Pred. No. 55;
                                                                                                                                                                                                                                                            210121.422C2
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RESULT 27
US-08-684-024-2
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OTHER INFORMATION: where any Xaa is an independently selected amino OTHER INFORMATION: acid
US-09-256-976-37
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APPLICANT: Smith, John M.
APPLICANT: McNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
TITLE OF INVENTION: OF T. CRUZI INFECTION
FILE REFERENCE: 210121.422C3
CURRENT FAPLICATION NUMBER: US/09/256,976
CURRENT FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
TENGREL 610
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Patent No. 64199
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Patent No. 5834298
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Benezra, Robert
TITLE OF INVENTION: GENE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 639
TYPE: PRT
ORGANISM: Trypanosoma cruzi
                                                                                                             APPLICATION NUMBER: US/08/684
FILING DATE: 19-UUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                 TELEFAX: (212) 391-0526:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acide
                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                    amino acid
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1185 Avenue of the Americas
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Pred. No.
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                                                                                                                                                       RESULT 29
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Patent No. 5834298
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                     Sequence 2, Application US/09145868
Patent No. 6096522
GENERAL INFORMATION:
APPLICANT: Benezia, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ANDRESSES
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                 Best Local Similarity
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APPLICANT: Benezr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Benezra, Robert TITLE OF INVENTION: GENE E
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1185 AVCITY: New York
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                  ADDRESSE:
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3: Cooper & Dunham LLP
1185 Avenue of the Americas
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46.7%; Pred. No.
                                                                                                                                                                                                                                                                                    38.2%;
46.7%;
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Pred. No. 20;
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20;
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                                                                                                                                                                                                                                                                                                     Length 196;
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STATE: New York COUNTRY: U.S.A.

New York

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TOPOLOGY: linear;
MOLECULE TYPE: protein US-09-145-868-2
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US-09-145-868-9
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ATTORNEY, AGENT INFORMATION:
NAME: White, John P. 28,678
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.2%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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                                                                                                                                                                                              COUNTRY: U.S.A.

ZIP: 10036

ZIP: 10036

COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30

SOPTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,868

FILING DATE: 02-SEP-1998

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMEER: 28,678
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0526
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ZIP: 1036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/145,868

FILING DATE: 02-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Benezra, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 196 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: U.S.A.
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Pred. No. 20;
                                                                                                                     1747/46621-B
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Search completed: May 4, 2004, 09:14:11 Job time : 15 secs

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Scoring table:
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Listing first 100 summaries
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    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 5100/, A Sequence 52954, A Sequence 52806, A	~	Sequence 3, Appri Sequence 37166, A	250163,	Sequence 250166,	nce		920	926	equence	Sequence 8187, Ap	equence	equence	equence	quence	sequence 194041, A			Sequence		Sequence 61839, A	Sequence 44862, A	Sequence 14, Appl	Sequence 1936, Ap	Sequence	Sequence 1539, Ap	Sequence 2, Appli	Sequence /, Appli	Sequence 2, Appli	Sequence 21, Appl	Sequence 21656, A	Sequence 211056,	Sequence	Sequence 457, App	٠.		Sequence 453/2, A Sequence 199858,	Sequence 49790,	43803,	Sequence 17, Appl	180,	117,	Sequence 2103,	37. Ac	7107	quence 41, App	quence 194106,	quence :	quence 53178,	quenc	equence 1	equence 2	equence 12456,	quence 55

Length 1475;

Indels

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Gaps

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RESULT 1
US-09-740-274-4
FILE REPERENCE: 0357CRD: US/09/740,274
CURRENT PELLING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR PELLING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/07,999
PRIOR PELLING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
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PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/00
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/47
PRIOR FILING DATE: 1995-06-07
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Patent No. US20020031826A1
                                                                                                                                                       Sequence 2, Application US/09740274
Patent No. US20020031826A1
GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
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CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
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TITLE OF INVENTION: Glucan-containing Compositions and Paper
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/009,620
PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 08/485,243
                                                                                                                                       APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions and Paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: streptococcus mutans
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2 US-10-425-114-46753
0 US-09-934-455-326
0 US-09-934-455-326
2 US-10-412-699B-870
2 US-10-225-066A-646
5 US-10-302-267-1198
5 US-10-374-780A-2598
2 US-10-374-780A-2598
2 US-09-920-954-4
2 US-09-815-242-14055
0S-09-815-242-14055
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Sequence 870, App
Sequence 646, App
Sequence 198, App
Sequence 2598, Ap
Sequence 4, Appli
Sequence 64570, A
Sequence 10095, A
Sequence 14055, A
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Sequence
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46753, A
326, App
       GENERAL INFORMATION:

APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA

APPLICANT: DIJKHUIZEN, LUBBERT

APPLICANT: LEER, ROBERT-JAN

APPLICANT: LEER, ROBERT-JAN

TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES

FILE REFERENCE: BO43388-CIP

CURRENT APPLICATION NUMBER: US/09/995,749A

CURRENT FILING DATE: 2001-11-29
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TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
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PRIOR APPLICATION NUMBER: 09/00
PRIOR PRILING DATE: 1996-01-20
PRIOR APPLICATION NUMBER: 08/48
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/00
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SEQ ID NO 11
LENGTH: 522
TYPE: PRT
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                                                                                                                                                               Sequence 13, Application US/09995749A Patent No. US20020155568A1
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APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
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TYPE: PRT
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1998: 08/482,711
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63.6%;
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                                                                                                                                     GERRITDINA HENDRIKA
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Pred. No. 3.9e-07
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Pred. No. 0.
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> DB 9; .00023;

Length 522;

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Indels

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Gaps

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PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 535
TYPE: PRI
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APPLICANT: UAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
APPLICANT: LEER, ROBERT-JAN
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT EILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR PILLING DATE: 2000-06-28
PRIOR PILLING DATE: 2000-05-25
PRIOR PILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Leuconostoc mesenteroides
US-09-995-749A-12
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 584
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APPLICANT: VAN GEEL-SCHUTTEN,
APPLICANT: DIJKHUIZEN, LUBBEH
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
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Best Local Similarity 63.2%;
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CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
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PRIOR FILING DATE: 2000-06-28
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167 IPNYSFVRAHDYDAQDPIR 185
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54.5%;
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 Mismatches

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Pred. No. 0.017;
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SEQ ID NO 2
LENGTH: 2057
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                  SEQ ID NO 10
LENGTH: 545
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                               Patent No. US20020155568A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
FILE REPERSNCS: 0147-0247P
CURRENT APPLICATION NUMBER: US/10/417,280A
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: DE 19905069.4
PRIOR APPLICATION NUMBER: US 09/499,203
PRIOR PILING DATE: 1999-02-08
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
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                                                                                                            CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                               APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: BO43388-CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 54
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ORGANISM: Lactobacillus reuteri
                                                                                                                                                                                                                                                                                                       APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
                                                                        SOFTWARE: PatentIn Ver. 2.1
                                                                                              NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 1781
ORGANISM: Streptococcus mutans
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Local Similarity 54.5%;
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Pred. No.
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Pred. No. 0.073;
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SEQ ID NO 6
LENGTH: 14
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Best Local Similarity
Matches 13; Conserv
                                                              NUMBER OF SEQ II
SEQ ID NO 168435
LENGTH: 117
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PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 1998-01-20
PRIOR APPLICATION NUMBER: 243
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CURRENT FILING DATE: 2000-12-19
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TITLE OF INVENTION: Glucan-c
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PRIOR APPLICATION NUMBER:
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PRIOR FILING DATE: 1998-12-11
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PRIOR APPLICATION NUMBER:
                                                                                               APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT SPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Kovalic David K
FEATURE:
NAME/KEY: unsure
                               ORGANISM: Glycine max
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Pred. No.
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Pred. No. 0.47;
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US-10-424-599-168435
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US-10-369-493-12332
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US-10-282-122A-76707
; Sequence 76707, Application US/10282122A
; Publication No. US20040029129A1
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12332
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Best Local Similarity 45.0%;
Matches 9; Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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OTHER INFORMATION: unsure at all Xaa locations
PRATURE:
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APPLICANT:
APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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                                                                                                                                                                                     APPLICANT:
                                                       APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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Local Similarity 40.9%; Pred. No. les 9; Conservative
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Malone, Cheryl
                                                                                                                                             Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                       Carr, Grant
                                                                                                                                                                                                                                                                                       Haselbeck,
                                                                                                                                                                                                            Trawick, John
                                                                                                                                                                                                                            Daniel
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                                                                                                                                                                                                                                                                                     Robert
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Pred. No. 7.5;
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; ORGANISM: Ureaplasma urealyticum
US-10-282-122A-76707
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US-10-282-122A-71700
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SEQ ID NO 76707
LENGTH: 597
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                      PRIOR PRIOR
                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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FILING DATE: 2000-09-06
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                                                                 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                      APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06 APPLICATION NUMBER: 60/230,347
                                                  APPLICATION NUMBER: 60/253,625
                                 FILING DATE:
                                                                                                       FILING DATE:
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                APPLICATION NUMBER: 60/257,931
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Zamudio, Carlo
Malone, Cheryl
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2000-12-22
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Pred. No.
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FEATURE: MISC FEATURE
LOCATION: (11)...(11)
COTHER INFORMATION: X=any amino acid
US-10-282-122A-71700
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US-10-424-599-232822
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_52263C.l.pep
US-10-424-599-232822
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LENGTH: 465
TYPE: PRT
ORGANISM: Staphylococcus haemolyticus
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2001-02-16
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Best Local
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 203-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 229462
                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                         Sequence 229462, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Cao Yongwe:
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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ORGANISM: Glycine max
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55.6%;
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Pred. No. 4
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US-10-424-599-159618
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US-09-815-242-5584
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Best Local Similarity 40.0%;
Matches 10; Conservative
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LENGTH: 170
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Best Local 9
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323)B
CURRENT FILING NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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LOCATION: (1)..(111)
OTHER INFORMATION: unsure at all Kaa locations
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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ORGANISM: Glycine
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LOCATION: (1)..(170)
OTHER INFORMATION: unsure at all Xaa locations
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7; Conserv
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Zhou Yihua
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                                                                                                                                             Wall, Daniel
Trawick, John D.
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Zyskind, Judith W.
                                                                                                                              Carr, Grant J.
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Pred. No. 17;
5; Mismatches 0; Indels
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US-09-815-242-12456
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                                                     ; ORGANISM: Staphylococcus aureus US-09-815-242-12456
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5584
                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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                                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12456
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011E US/09/815,242 CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR TILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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TYPE: PRT
ORGANISM: Staphylococcus aureus
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                                                                                                TYPE: PRT
                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12456, Application US/09815242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
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Pred. No. 68;
Score 45.5;
Pred. No. 69;
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Best Local Similarity

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DB 9;

Query Match

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US-10-424-599-264904
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LENGTH: 166
                                                                    Matches
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LENGTH: 171
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                                                                                                    Query Match
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT EPPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                    APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David
                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT_MRT3847_137365C.1.pep
                                                                                                                                                                             ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                   TYPE: PRT
                                                                                     Local Similarity
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37
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                                SYSFARAHDSEVODLIRDI 21
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THSFLSDHRSDYEDFLRDI 55
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Zhou Yihar
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ilarity 42.1%;
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                                                                    Score 45; DB Pred. No. 25; Signature 5; Mismatches
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Pred. No.
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3; Mismatches
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                                                                                                                                         ; OTHER INFORMATION: Clone US-10-424-599-250160
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Best Local
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LENGTH: 362
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SEQ ID NO 250160
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                                                                     Matches
                                                                                       Query Match
Best Local
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Cao Yongwel
TITLE OP INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT EPPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1)..(365)
OTHER INFORMATION: unsure at all Xaa locations
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LOCATION: (1)..(362)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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ORGANISM: Glycine
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                                PSYSFARAHDSEVODLIRDI 21
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 PGMDMPIMHDSDRYDLVRDI 29
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Pred. No.
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                                                                       Score 45; DB Pred. No. 60; 2; Mismatches
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RESULT 25
US-10-425-114-65612
; Sequence 65612, Application US/10425114
; Publication No. US20040034888A1
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: On INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53178
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Jingdong
APPLICANT: Zbou, Yihua
APPLICANT: Screen, David
APPLICANT: Screen, Steven
APPLICANT: Tabaska, Jack:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 50726
LENGTH: 414
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Best Local
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                                                                                                                            64 PGMDMPIMHDSDRYDLVRDI 83
                                                                                                                                                                                                 n 40.9%;
Similarity 45.0%;
9; Conservative
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                 PSYSFARAHDSEVODLIRDI 21
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Pred. No. 62;
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Pred. No.
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APPLICANT: LOU, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 65612

LENGTH: 423

TYPE: DPT
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US-10-424-599-194106
        US-10-334-143-41

Sequence 41, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT GRIGORIEV, IGOR VYACHESLAVOVICH

APPLICANT GRIGORIEV, GUTCHE
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                                                                                                         RESULT 27
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 194106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 194106, Application US/10424599
publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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Best Local Similarity 42.9%;
Matches 9; Conservative
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NAME/KEY: unsure
LOCATION: (1)..(963)
OTHER INFORMATION: v
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FEATURE:
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SUDARSANAM, SUCHA
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Pred. No. 71;
4; Mismatches
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Pred. No. 1.9e+02;
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CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 71074
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PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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ORGANISM: Staphylococcus epidermidis 10-282-122A-71074
                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Local Similarity 47.18;
nes 8; Conservativo
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APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                          FILING DATE: 2000-12-22
                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/257,931
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Malone, Cheryl
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Zyskind, Judith
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Pred. No. 5.9e+02;
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                                                                                                                        ; ORGANISM: Homo sapiens US-09-862-027-37
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US-09-862-027-37
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APPLICANT: La ROSE Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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SEQ ID NO 267457
LENGTH: 115
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Best Local Similarity
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Matches 7; Conserv
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APPLICANT: Hodge, Martin R.
                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application Upatent No. US20020142428A1
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                                                                                        Query Match
                                                                                                                                                                                                             TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof FILE REFERENCE: 35800/234862 CURRENT APPLICATION NUMBER: US/09/862,027 CURRENT FILING DATE: 2001-05-21 PRIOR APPLICATION NUMBER: US 09/345,473 PRIOR FILING DATE: 1999-06-30 NUMBER: 05 SEQ ID NOS: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
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CURRENT FILING DATE: 2003-04-28
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NAME KEY: unsure

LOCATION: (1)..(115)

OTHER INFORMATION: unsure at all Xaa locations

PEATURE:

PEATURE:
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                                                                                                                                                      LENGTH: 3
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 190 SPEKVHDPEIKEIIGECI
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Match
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Matches
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                                                                                                                                                                                                                                                 The present sequence is the protein sequence of Streptococcus downer glucosyltransferase-S (GTF-S). Peptide fragments of GTF-S, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II protein-binding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucosyltransferase; enzyme; vaccine; anticaries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD93659 standard; protein; 1365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus downei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus downei glucosyltransferase-S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 15-16; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-845091/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2003; 2003WO-US006962.
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                                                                                                                                                                                                                              Sequence 1365 AA;
 27-AUG-2002
                                                     AAU98036 standard;
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lass II protein.
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                                                                                                                                             1 VPNYVFIRAHDSEVQTRIAKII 22
                                                                                                                                                                          22;
                                                                                                                                                                                        Similarity
                                                                                                                      VPNYVPIRAHDSEVQTRIAKII 558
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961
                                                     protein; 1475 AA
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ABG76429
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                                                                                                                                                                                        Score 110; DB 7;
Pred. No. 1.8e-10;
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                                                                                                                                                                           Mismatches
                                                                                                                                                                                                       DB 7;
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                                                                                                                                                                                                      Length 1365;
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Abg76429 Brome mos
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07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                 Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic amyloplast; vacuole; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans
                                                                                                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                                                                         19-DEC-2000; 2000US-00740274
                                                                                                                                                                                                                                                                                                                                     14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                 US2002031826-A1.
                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                            (NICH/) NICHOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                           mutans glucosyltransferase GTFB mutant D567T/D571K
                                                                                                                                                                                                                                                                       95US-00482711.
95US-00485243.
98US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 567
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                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type Asp substituted by Lys"
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                                                                                                                                                                                                                                                                                                                                                                                                                            molecule;
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Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions. a glucan useful latexes in pape paper

WPI; 2002-414332/44

Claim 36; Page; 44pp; English.

cc R polypeptide having changes at position from 148V, D457N, D5677, D457N/D5677, D457N/D5677, D457N/D571K, D5677/D571K, D5677/D571K, D5677/D571K, D6677/D571K, M610447, M64074, M640

biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer

the GTFB sequence appearing as AAU98027 and the information

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11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glucosyltransferase; coating composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. mutans glucosyltransferase GTFB mutant D567T/D571K/K1014T
                                                            Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in pape manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU98037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU98037 standard; protein; 1475 AA.
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The invention an isol
B polypeptide having
K1014T, D457N/D567T,
                                                                                                                                                                                                                                                                                                                                                                                                                                               amyloplast;
                                          Claim 36;
                                                                                                                               Nichols
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPNYVFIRAHDSEVOTRIAKII 22
                                         Page; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               vacuole;
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                                                                                                                                                                                                                                                              2000US-00740274.
an isolated protein comprising a glucosyltransferase
having changes at position from I448V, D457N, D567T,
/D567T, D457N/D571K, D567T/D571K, D567T/D571K/Kl014T,
                                                                                                                                                                       95US-00485243.
98US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
                                                                                                                                                                                                                               95US-00478704.
95US-00482711.
                                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Asp
1014
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                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Lys
                                                                                                                                                                                                                                                                                                                                                                      note= "Wild-type Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule; paper manufacture; mutant; mutein.
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86.4%;

    Mismatches

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Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                                                            substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                  substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                       substituted by
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Sequence 1475 A

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                                     Query Match
Best Local Similarity
Matches 19; Conserv
           VPNYVFIRAHDSEVQTRIAKII 22
 VPSYSFIRAHDSEVQTLIAKII 573
                                      Conservative
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                                      Mismatches
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3.7e-07;
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AAU98038 standard; protein; 1475 AA
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AAU98038; (first entry)

27-AUG-2002

S. mutans GTFB mutant I448V/D457N/D567T/D571K/K779Q/K1014T

Glucosyltransferase; GTPB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein. mutans

Streptococcus Synthetic.

RESULT 4
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The invention an isolated protein comprising a glucosyltransferase (GTF) CC Hypeptide having changes at position from 1448V, D567T, D57TK, D567T, D57TK, K1014T, D67T/D57TK, D567T/D57TK, K1014T, CC H148V/D457N/D567T/D57TK/K719Q/K1014T, Y169A/Y10A/X17JA, and K779Q or a CC GTF D polypeptide having changes at positions from T589D, T589E, M471D, CC GTF D polypeptide having changes at positions from T589D, T589E, M471D, CC GTF muttant, an isolated polynucleotide which encodes P1 or P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the CC GTF muttant, an expression cassette comprising the polynucleotide operably CC linked to a promoter, a vector comprising the polynucleotide operably CC coating composition comprising a glucan produced in the condens of the condens of the condens of the condens of the composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, conditions of producing the mutant GTF, wild type or starch, a latex, conditions of producing a glucan in the amyloplast and/or vacuole or a maize line comprising the glucan in a plant. The wettor is useful comprising the glucan in a plant. The wettor is useful comprising the glucan in a plant. The wettor of the plant and inducing expression of the conditions to produce a regenerated plant and inducing expression of the conditions of the polynucleotide for a time sufficient to produce the glucan in the conditions of the conditions of the conditions of the sufficient of produce a transforming and glucan in the amyloplast of potating expression of the conditions are useful as substitutes for and additions to modified starch of the conditions are useful as substitutes for and additions to modified starch where the vector or and additions to modified starch of the vacuole of sugar beet.

CC and latexes in paper manufacture. Unlike prior art techniques, which
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20-JAN-1998;
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                                                                    and latexes in paper manufacture. Unlike prior art techniques, which and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 36; Page; 44pp; English
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Sequence 1475

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Length 1475;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bloactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the pharmaceutical compositions intended for improving the condition of the contaction of the state of the condition of the contaction of the
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N-PSDB; ACC50074.
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25-JUL-2001; 2001EP-00202841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucansucrase gene
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                                                                                                               ABR63228 standard; protein; 223
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener
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25-JUL-2001; 2001EP-00202841.
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                                                                                                                                                                                                                                    Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal
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22-JUL-2002; 2002WO-NL000495
                                                                                                                     WO2003008618-A2
                                                                                                                                                                           Lactobacillus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR63227 standard; protein;
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                                                                                                                                                                                                                                 agent;
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                                                                                                            07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
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25-JUL-2001; 2001EP-00202841.
                         16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. mutans glucosyltransferase GTFD mutant N471D.
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95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
                                                                                                                                                                                                                                                                                                                                                                                                                  471
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTFD; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule;
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1; Mismatches
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98US-00210361

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complementary polynucleotice, a ribonucleur sequence encounty the coll inked to a promoter, a vector comprising the polynucleotide operably cell introduced with the vector, a transgenic plant, a paper sixing and/or vector, a seed or tuber from the transgenic plant, a paper sixing and/or coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTP, wild type or, starch, a latex, cell the glucan is produced in the amyloplast and/or vacuole or a maize line deficient in starch biosynthesis, transformed with a gene encoding a glucan (paper sizing/coating agent). The vector is useful comprising the glucan (paper sizing/coating agent). The vector is useful cell polynucleotide for a time sufficient to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the plant cell under plant growing to glucans are useful as substitutes for antains a transit sequence from cell under plant, where the vector contains a transit sequence from chlorophyll AB binding protein to produce a transgenic plant, and glucan cell under plant, and glucan cell under spant and substitutes for and additions to modified starch cell under spant and plant, and glucan and latexes in paper manufacture. Unlike prior art techniques, which cell conditions to modified starch cell biologically produced input materials, is more cost-effective and cell properties and impart gloss to the paper during coating step. The present cell sequence represents a GTFD matant of the invention. Note: The present cell using the GTFD sequence appearing as AAU98029 and the information in
RESULT 9
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in pape manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-414332/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1430 AA
                      S. mutans glucosyltransferase GTFD.
                                                                                                                                                  AAU98029 standard; protein; 1430 AA
                                                                 27-AUG-2002
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                                                                                                                                                                                                                                                                576
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                                                                   (first entry)
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16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
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16-JAN-1998;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                          14-MAR-2002
                                                                                                                                                                                                                                  (NICH/) NICHOLS
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95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-0009620.
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Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions. a glucan useful latexes in pape

N-PSDB;

ABK52940

Page 38-42; 44pp; English.

The invention an isolated protein comprising a glucosyltransferase (GTF) CC K1014T, b457N/D567T, b457N/D571K, D567T/D571K,
Sequence 1430 AA;

Best Local Similarity Query Match 81.8%; 90.0%; Score Pred. 90; DB 5; 8.2e-07; Length 1430;

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Best Local S
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the protein sequence of Streptococcus mutans glucosyltransferase-D (GTF-D). Peptide fragments of GTF-D, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II protein-binding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful as vaccines for a glucan binding protein-B binding class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glucosyltransferase; enzyme; vaccine; anticaries; epitope; immunogen.
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                                         ABR63234;
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  27-AUG-2003
                                                                                 ABR63234 standard;
                                                                                                                                                                                                                                                                                                                                                          Sequence 1430 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 13-14; 49pp; English
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bloactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
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25-JUL-2001; 2001EP-00202841.
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                                                                                                                                                                                                                                                                             Dextran saccharase; enzyme; cytostatic; dermatological; antiseborrheic; DSR-B; glycosyl transferase; dextran; prebiotic; pharmaceutical; microflora regulation; intestinal transit; mineral assimilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dextran saccharase,
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14-JAN-2003
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        /label= Signal_peptide
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Peptide
The present sequence is a novel dextran saccharase, DSR-E, rrom Leuconostoc mesenteroides NRRL B-1299. The saccharase has glycosyl transferase activity suitable for producing dextrans having alpha(1-2) branches from sucrose, p-nitrophenyl-alpha-D-glocopyranoside, alpha-fluoroglucose, alpha-D-glucopyranoside-alpha-D-sorbopyranoside or alpha-glactopyranosyl-sucrose. The dextran saccharase is useful in prebiotic, pharmaceutical or commetic compositions. The dextrans and related compounds having alpha(1-2) bonds, produced using DSR-E, may be involved in signalling/cellular recognition processes in vivo (specifically in in signalling/cellular recognition processes or on the skin); and are
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/note= "Catalytic domain, SEQ
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Best Local S
Matches 18
                 The present sequence represents a glycosyltransferase, designated DSR-D. This enzyme produces dextrans having alpha(1-2) branches from sucrose, alpha-D-fluoroglucose, p-nitrophenol alpha-D-glucopyranoside, alpha-D-glucopyranoside alpha-D-sorbofuranoside or 4-O-alpha-D-glucopyranosylsucrose. The polypeptide is used to prepare oligosaccharides and oligosides for prebiotic, pharmaceutical, diagnostic and cosmetic applications, e.g. to improve health and weight gain in animals; prevent cancer of the colon; and treat skin disorders such as acne, dandruff and body odour. The oligosaccharides and oligosides produced by DSR-D improve intestinal transit and assimilation of calcium, magnesium and other minerals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-D-fluoroglucose; p-nitrophenol alpha-D-glucopyranoside; alpha-D-glucopyranoside-alpha-D-sorbofuranoside; oligosaccharide; oligoside; 4-O-alpha-D-galactopyranosylsucrose; weight gain; colon cancer; skin disorder; acne; dandruff; body odour;
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                                                                                                                                                                                                         New polypeptide with glycosyltranaferase activity, useful dextrans with alpha 1-2 branches, e.g. used as prebiotics
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N-PSDB; ACC70331.
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problems such as a
3 to standardise OS
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Query Match Best Local S Matches 18

Similarity

81.8%;

Score 90; Pred. No. 1; Mismatc

DB 6, 1.9e-06; 2;

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Gaps

0;

Length 2835

Mismatches

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RESULT 15
ADC54807
ID ADC54
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                                                                                                                             Matches
                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                              infant formulae and pet foods. Dextransucrase can also be bound to eg. vitamins or oral vaccines for delivering these to foods, using (A) as carrier. The method produces foods with attractive and uniform texture, since dextransucrase is evenly distributed and forms a thickening agent in situ, with the amount formed being controlled by the amount of dextransucrase bound. Milk does not have to be coagulated in order to achieve a good texture, so the amount of acidic by-products formed is reduced. Dextransucrase binds to many different types of cells over wide ranges of temperature and pH and the treated bacteria can be stored in liquid or powdered form. The present sequence represents the amino acid sequence of dextransucrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1201131-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dextransucrase; yoghurt; curd; cheese; fermented milk; infant formulae; pet food; vitamin; oral vaccine; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU80055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU80055
                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to preparation of a fermented food product that includes treating the microorganism (A) to be used for fermentation with a dextransucrase so that this binds to the cell walls of (A). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 14-20; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing fermented food I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK50932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bauche A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2000; 2000EP-00123012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leuconostoc mesenteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leuconostoc mesenteroides dextransucrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-2000; 2000EP-00123012
   ADC54807 standard; protein; 1527
                                                                                                                                                                                         Sequence 1527 AA;
                                                                                                                                                                                                                                                                                                                                                                                            is used to produce yoghurt, curd, cheese or other fermented milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEST )
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                                                                                                  1 VPNYVFIRAHDSEVQTRIAKII 22
                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   texture.
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                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNYVFIRAHDSEVQTRIAKII 22
                                                                          IPNYSFVRAHDSEVQTVIAQIV 673
                                                                                                                                                                                                                                                                                                                                                                                  ice cream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Maleprade D,
                                                                                                                                Conservative
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                                                                                                                                              80.9%;
                                                                                                                                                                                                                                                                                                                                                                                  fermented cereal products, water-based jellies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products, e bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duboc P, Neubauer H,
                                                                                                                                4
                                                                                                                                Score 89; DB 5;
Pred. No. 1.4e-06;
4; Mismatches 2
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the surface, p
                                                                                                                                                               DB 5;
                                                                                                                                   <u>ب</u>
                                                                                                                                                               Length 1527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , using microorganisms provide attractive and
                                                                                                                                   Indels
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RESULT 16
ADC546
ID ADC54
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AC ADC54
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DT 18-DE
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EN dext1
KW dext1
KW D-gl1
KW enzyn
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OS Unide
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DF206
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a modified dextran sucrase (DS) exchanging one site of the active centre zone of a dextran sucrase for the active centre zone of different types of dextran sucrase. Glucan is a polysaccharide (for example dextran) which uses D-glucoses, such as a starch and a cellulose, as a structural unit. The modified enzyme of the invention is useful in the manufacture of glucan. The selection of the active centre area of DS which carries out transduction, enables changes in structure and character of an enzyme-reaction product and their application to various uses. The present sequence is that of the Leuconostoc mesenteroides dextran sucrase protein used during the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel modified dextran sucrase which exchanges one site of active zone of dextran sucrase for active center zone of different types dextran sucrase, useful for manufacturing glucan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dextran sucrase; active centre zone; glucan; polysaccharide; dextran; D-glucose; starch; cellulose; glucan manufacture; transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC54807;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme-reaction product.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 12; 28pp; Japanese.
                                                                                      dextran sucrase; active centre zone; glucan; polysaccharide; de D-glucose; starch; cellulose; glucan manufacture; transduction;
                                                                                                                                   Protein Seq ID11 related to L mesenteroides dextran sucrase protein.
                                                                                                                                                                   18-DEC-2003
                                                                                                                                                                                                 ADC54806
                                                                                                                                                                                                                            ADC54806 standard; protein; 1499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention.
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                                                                         enzyme-reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-735670/70.
                                                                                                                                                                                                                                                                                                         652 IPNYSFVRAHDSEVOTVIAQIV 673
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                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                   (first entry)
                                                                            product.
                                                                                                                                                                                                                                                                                                                                                                                  80.9%;
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Pred. No.
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JP2003111590-A

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RESULT 17
ADD93658
ID ADD93658
XX ADD93658
AC ADD93
XX GDD9
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a modified dextran sucrase (DS) exchanging one site of the active centre zone of a dextran sucrase for the active centre zone of different types of dextran sucrase. Glucan is a polysaccharide (for example dextran) which uses D-glucoses, such as a starch and a cellulose, as a structural unit. The modified enzyme of the invention is useful in the manufacture of glucan. The selection of the active centre area of DS which carries out transduction, enables changes in structure and character of an enzyme-reaction product and their application to various uses. The present sequence is that of a protein which is related to the Leuconostoc mesenteroides dextran sucrase protein and which was used during the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel modified dextran sucrase which exchanges one site of active zone of dextran sucrase for active center zone of different types dextran sucrase, useful for manufacturing glucan.
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                      Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus sobrinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucosyltransferase; enzyme; vaccine; anticaries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus sobrinus glucosyltransferase-U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD93658 standard; protein; 1554 AA
                                                                                                                                                                                                                                                                                                          07-MAR-2002;
08-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2003; 2003WO-US006962
                                                                                                                                         WPI; 2003-845091/78
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                                                                                                                                                                                                                                                         (FORS-) FORSYTH INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNYSFVRAHDSEVOTVIAEII 645
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                                                                                                                                                                                                                                                                                                          2002US-0363209P
2002US-0402483P
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81.0%;
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Pred.
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No.
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3.1e-06;
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RESULT 18
AAU98035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the protein sequence of Streptococcus sobrinus glucosyltransferase-U (GTF-U). Peptide fragments of GTF-U, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II proteinbinding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                        07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic amyloplast; vacuole; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. mutans glucosyltransferase GTFB mutant D457N/D571K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU98035 standard; protein; 1475
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                                                                                                                                                                                                                                                                                                                                    Misc-difference 571
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
Misc-difference 457
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans
                                                                                                                                                                                                                                                                      14-MAR-2002
                                                                                                                                                                                                                                                                                               US2002031826-A1
                                                                                                                                                                                                                                             19-DEC-2000; 2000US-00740274
                                                                                         Nichols
                                                                                                                 (NICH/)
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                                                                 2002-414332/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 72.7
16; Conservative
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                                                                                                                                         95US-00478704.
95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
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72.7%;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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3.2e-06;
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                                 a glucan useful
latexes in pape
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Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.

paper

Claim 36; Page; 44pp; English

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RESULT 19
AAU98034
ID AAU98
XX AAU98
AC AAU98
AC AAU98
AC AAU98
XX 27-AL
XX 27-AL
XX Glucc
XW Glucc
XW Coati
XW coati
XW amylc
XX Synth
XX Misc
FT Misc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC GTF mutant, an isolated polynucleotide which encodes plor P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the CC GTF mutant, an expression cassette comprising the polynucleotide operably CC linked to a promoter, a vector comprising the polynucleotide operably CC linked to a promoter, a vector comprising the polynucleotide operably CC linked to a promoter, a vector comprising the polynucleotide operably CC linked to a promoter, a vector, a transgenic plant comprising and/or cell introduced with the vector, a transgenic plant comprising and/or coating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTF, wild type or, starch, a latex, CC thermoplastic molecule or thair combinations or glucan and starch where the glucan is produced in the amyloplast and/or vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a CC glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC comprising the glucan (paper sizing/coating agent). The vector is useful CC comprising the glucan in a plant The method comprises transforming a CC plant cell with the vector, growing the plant cell under plant growing CC conditions to produce a regenerated plant and inducing expression of the CC polynucleotide for a time sufficient to produce the glucan in the composition to produce a transit sequence from CC chlorophyll AB binding protein to produce a transit sequence from CC conditions are useful as substitutes for and additions to modified starch cc properties and impart gloss to the paper during costing the green which CC properties and impart gloss to the produced by GTF, which utilises biologically produced input materials, is more cost-effective and CC properties and impart gloss to the paper during costing step: The present counting the GTFB mutant of the invention. Note: The present counting the GTFB sequence appearing as AAU98027 and the information in
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                                                                                                                                                                                                                                                                           S. mutans glucosyltransferase GTFB mutant D457N/D567T
                                                                                                                                                                                                            Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1475 AA;
                                                                                                                                          Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAU98034 standard; protein; 1475
  Misc-difference
                                              Misc-difference
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                                              Location/Qualifiers
    /note= "Wild-type Asp substituted by 567
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81.8%;
                                                                                                                                                                                        paper
                                                                                                                                                                                           manufacture; mutant; mutein.
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Pred. No. 4.6e-06;
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07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
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                                                                                                                                                                                        95US-00478704.
95US-00482711.
95US-00485243.
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98US-00009620.
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Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions. a glucan useful latexes in paper in paper

Claim 36; Page; 44pp; English.

CC GTF mutant, an isolated polymucleotide which encodes ploor producing the complementary polymucleotide, a ribonucleic acid sequence encoding the CC GTF mutant, an expression cassette comprising the expression cassette, host CC linked to a promoter, a vector comprising the expression cassette, host CC coating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTF, wild type or, starch, a latex, CC with a gene encoding the mutant GTF, wild type or, starch, a latex, CC with a gene encoding the mutant GTF, wild type or, starch, a latex, CC with a gene encoding the mutant GTF, wild type or, starch, a latex, CC with a gene encoding the mutant GTF, wild type or starch where CC deficient in starch biosynthesis, transformed with a gene encoding a glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC comprising the glucan (paper sizing/coating agent). The vector is useful CC planticient by producing a glucan in a plant. The method comprises transforming a CC comprising the producing a plant. The plant cell under plant growing CC comprising the produce a regenerated plant and inducing expression of the CC polymucleotide for a time sufficient to produce the glucan in the CC plucans are useful as substitutes for and additions to modified starch comprises in paper manufacture. Unlike prior art techniques, which cc manufacture utilising the glucan produce by GTF, which utilises biologically produced input materials, is more cost-effective and cc properties and impart gloss to the paper during coating step. The present sequence is not shown in the specification but was created by the indexer sequence is not shown in the specification but was created by the indexer sequence is not shown in the specification but was created by the indexer sequence is not shown in the specification but was created by the indexer sequence is not shown in the specification but was created by the indexer sequence is not shown in the specification but was created by the indexer sequenc The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from 1448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T, D577N/D571K/X1014T, K1014T, V169A/Y170A/Y171A, and K779Q or a I448V/D457N/D567T/D571K/K779Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D, GTF D polypeptide having changes at positions from T589D, T589E, N471D, 1448V/D457W/D567T/D57LK/K/19V/KLUZZ, 1400V/D457W/D567T/D57LK/K/19V/KLUZZ, 1400V/D457W/D589D, T589E, N471D, GTF D polypeptide having changes at positions from T589D, T589E, N471D, N471D/T589D, and N471D/T589E. Also included are a glucan produced by the management of the second secon the GTFB sequence appearing 36 as AAU98027

Sequence B

Query Match Best Local Similarity Conservative 81.8%; 1; Mismatches Score 86; DB 5; Pred. No. 4.6e-06; Length 1475; 0, Gaps

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RESULT 20
AAU98032
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The invention an isolated protein comprising a glucosyltransferase (GTF) The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from 1488V, D457N, D567T, CK K1014T, D457N/D571K, M567T/D571K, M5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucosyltransferase; coating composition;
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20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page; 44pp; English.
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95US-00485243.
98US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
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07-JUN-1995;
07-JUN-1995;
07-JUN-1998;
16-JAN-1998;
20-JAN-1998;
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                                                                                                                                                                   NICHOLS S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-00740274.
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95US-00482711.
95US-0048273.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Wild-type Asn substituted by Asp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.2%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTFD mutant
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Glucosyltransferase WPI; 2002-414332/44.

W e U

protein useful for producing a glucan useful

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CC The invention an isolated protein comprising a glucosyltransferase (GTF)
CC B polypeptide having changes at position from 1448V, D457N, D557T,
CC X1014T, D457N/D557T, D457N/D571K, D557T/D571K, X1014T,
CC Y418V/D457N/D567T,D571K/K779Q/K1014T, X169A/Y170A/Y171A, and K79Q or a
CC GTF mutant, an isolated polymuclectide which encodes P1 or P2, or its
CC complementary polymuclectide, a ribonucled are a glucan produced by the
CC GTF mutant, an isolated polymuclectide which encodes P1 or P2, or its
CC complementary polymuclectide, a ribonucled acid sequence encoding the
CC complementary polymuclectide, a ribonucled acid sequence encoding the
CC conting composition comprising the expression cassette, host
CC coating composition comprising glucan produced in a plant transformed
CC coating composition comprising splucan produced in a plant transformed
CC with a gene encoding the mutant GTF, wild type or, starch, a latex,
with a gene encoding the mutant GTF, wild type or, starch, a latex,
CC the glucan is produced in the amyloplast and/or vacuole or a maize line
CC deficient in starch biosynthesis, transformed with a gene encoding a
CC glucan is produce or bearing coating agent). The vector is useful
CC complicions to produce a regenerated plant and inducing expression of the
CC golymuclectide for a time sufficient to produce the glucan in the
CC polymuclectide for a time sufficient to produce a transgenic plant growing
CC plant cell with the vector, growing the plant cell under plant growing
CC plant cell with the vector, growing the plant and inducing expression of the
CC glucans are useful as substitutes for and additions to modified starch
CC is produced in the amyloplast of potato or the vacuole of sugar beet.
CC glucans are useful as substitutes for and additions to modified starch
CC is produced in the amyloplast of potato or the vacuole of sugar beet.
CC glucans are useful as substitutes for and additions to modified starch
CC is produced in the amyloplast of potato or the vacuole of sugar beet.
CC glucans are s
RESULT 22
AAU98045
ID AAU98045
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Best Local S
Matches 17
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                                                                                                                   Glucosyltransferase; coating composition;
                                                                                                                                                                      S. mutans glucosyltransferase GTFD mutant N471D/T589E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1430 AA;
                                      Synthetic
                                                          Streptococcus
                                                                                                                                                                                                                  27-AUG-2002
                                                                                                                                                                                                                                                                                         AAU98045 standard; protein; 1430
                                                                                               amyloplast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NYVFIRAHDSEVQTRIAKII 22
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                                                                                                 vacuole;
                                                                                                                                                                                                                  (first entry)
                                                            mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.4%;
                                                                                                                   GTFD; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule;
                                                                                                 paper
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                                                                                                   manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84; DB
Pred. No. 1e-0
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified starch and latexes in paper specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
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Location/Qualifiers

Query Match

76.48;

Score

84;

DB ú

Length 1430;

Sequence 1430

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The invention an isolated protein comprising a glucosyltransferase (GTF) CC Hoplypeptide having changes at position from 1488V, D457N, D557T, D457N/D567T, D457N/D571K, D567T/D571K/K1014T, CC K1014T, D457N/D567T,D571K/K1014T, D567T/D571K/K1014T, D667T/D571K/K1014T, D667T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D571K/E007T/D57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-2000; 2000US-00740274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in pape manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NICH/)
                                                                      environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence represents a GTFD mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L6-JAN-1998;
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                                       the GTFD sequence appearing
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                                                                as
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                                                                    the
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RESULT 23
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The invention an isolated protein comprising a glucosyltransferase (GTF) CC Hypeptide having changes at position from I448V, D457N, D567T, D457N/D571K, D567T/D571K, D567T/D571K/K1014T, CC I1448V/D457N/D567T, D457N/D571K, D567T/D571K/K1014T, CC GTF D polypeptide having changes at positions from T589D, T589E, M471D/T589D, and M471D/T589D. Also included are a glucan produced by the CC GTF muttant, an isolated polymucleotide which encodes Pl or P2, or its complementary polymucleotide, a ribonucleic acid sequence encoding the CC GTF mutant, an expression cassette comprising the polymucleotide operably CC linked to a promoter, a vector comprising the expression cassette, host cell introduced with the vector, a transgenic plant comprising the vector, a seed or tuber from the transgenic plant, a paper sizing and/or coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, the composition condecing the composition comprising a glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising as glucan produced in a plant transformed composition comprising the composition comprising the composition comprising the composition comprising the composition comprising the composition composition comprising the composition comprising the composition 
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16-JAN-1998;
20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002031826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-414332/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 NYIFIRAHDSEVQEVIAKII 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NICHOLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Thr substituted by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTPD; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1430
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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l latexes i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n useful
in paper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc comprising the glucan (paper sixing/coating agent). The vector is useful for producing a glucan in a plant. The method comprises transforming a cc plant cell with the vector, growing the plant cell under plant growing cc conditions to produce a regenerated plant and inducing expression of the cripulose biphosphate carboxylase small subunit, waxy, brittle-1 and cc ribulose biphosphate carboxylase small subunit, waxy, brittle-1 and cc chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. cc glucans are useful as substitutes for and additions to modified starch cc and latexes in paper manufacture. Unlike prior art techniques, which crequire input materials that produce chemical effluents, paper convironmentally produced input materials, is more cost-effective and comproduced imput materials, is more cost-effective and comproduced input materials, is more cost-effective and compromentally friendly. Moreover, glucans also exhibit thermoplastic environmentally friendly mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer cost in the cost of the invention in the information in
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                                                                                                                        07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucosyltransferase; GTFD; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S. mutans glucosyltransferase GTFD mutant T589D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU98041 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU98041;
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-2002
                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                     14-MAR-2002.
                                                                                                                                                                                                                                                                                                     US2002031826-Al
                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                    19-DEC-2000; 2000US-00740274
                                              Nichols SE;
                                                                            (NICH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the GTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 NYIFIRAHDSEVQEVIAKII 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
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                                                                              NICHOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYVFIRAHDSEVOTRIAKII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                          95US-00478704.
95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 589
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                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Thr substituted by Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 1430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 84; DB
Pred. No. 1e-0
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
le-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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WPI; 2002-414332/44

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The invention an isolated protein comprising a glucosyltransferase (GTF) CC B polypeptide having changes at position from 1448V, D457N, D567T, D457N, D567T, D571K, M104T, D567T/D571K, M104T, D567T/D571K, M104T, CC GT48V/D457N, D567T/D57TK, M104T, M163N/M104T, M163N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. Glucans are useful as substitutes for and additions to modified starch and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and biologically friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence represents a GTFD mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer series and the step of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 36; Page; 44pp; English
                                                                                                  Glucan, glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
                                                                                                                                                                                                                                   23-OCT-2003
27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1430 AA
                                                                                                                                                                             Glucansucrase sequence from
                                                                                                                                                                                                                                                                                                                ABR63235;
                                                                                                                                                                                                                                                                                                                                                              ABR63235 standard; protein;
                                                     Lactobacillus sakei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           576 NYIFIRAHDSEVODVIAKII 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NYVFIRAHDSEVOTRIAKII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
                                                                                                                                                                                                                                                                                                                                                                      2055 AA
                                                                                                                                                                                        strain KG15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84; DB 5;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1430;
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latexes in pape
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RESULT 26
ABR63229
ID ABR6329
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the products of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a sequence of the glucansucrase gene. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van
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25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-2002; 2002WO-NL000495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3) - and alpha (1,6)-linked anhydroglucose units, useful as thickener.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucansucrase sequence from strain Lb86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastroint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR63229 standard;
  WPI; 2003-289780/28
N-PSDB; ACC50073.
                                                                                                                                                                                            20-JUL-2001; 2001EP-00202752.
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                                               22-JUL-2002; 2002WO-NL000495
                                                                                  Van Geel- Schutten GH;
                                                                                                                                                                                                                                                                                                                                                                                               WO2003008618-A2
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Pred. No. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastrointestinal tract.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3) - and alpha (1,6)-linked anhydroglucose units, useful as thickener.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucan;
The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dair products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional
                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001EP-00202752:
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003008618-A2
                                                                                                                                                                              Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3) - and alpha (1,6)-linked anhydroglucose units, useful as thickener.
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                                                                                                                                             Claim 11; Fig 1; 51pp; English.
                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                           Geel- Schutten
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ve agent; anti-corrosion agent; foodstuff; gastrointestinal tract
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Pred. No.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU98031 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus mutans Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucosyltransferase;
The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from 1448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T/D571K/K1014T, K1014T, D457N/D567T/D571K/K779Q/K1014T, 1469A/K170A/K171A, and K779Q or a 1448V/D457N/D567T/D571K/K779Q/K1014T, 1469A/K170A/K171A, and K779Q or a 1750 D polypeptide having changes at positions from T589D, T589E, N471D, N471D/T589E. Also included are a glucan produced by the N471D/T589D, and N471D/T589E. Also included are a glucan produced by the Complementary polynucleotide which encodes P1 or P2, or its complementary polynucleotide polynucleic acid sequence encoding the Complementar, an expression cassette comprising the polynucleotide operably linked to a promoter, a vector comprising the expression cassette, host linked to a promoter, a vector comprising the expression cassette, host cell introduced with the vector, a transgenic plant comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coating composition;
amyloplast; vacuole;
                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                     Glucosyltransferase B or D protein useful for as substitutes for and additions to modified manufacture, comprises mutations in specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
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20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                               manufacture,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217
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PSYSFVRAHDSEVQTVIABIV 237
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                                                                                                                                                                                                                                                                                                                                                                  comprises mutations
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98US-00009620.
98US-00210361.
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98US-00007999.
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95US-00482711.
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                                                                                                                                                                                                                                                                                                                  44pp; English.
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glucan; starch; latex; thermoplast
paper manufacture; mutant; mutein.
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thermoplastic
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                                                                                                                                                                                                                                                                                                                                                                                                     a glucan useful
latexes in pape:
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ce the glucan is produced in the amyloplast and/or vacuole or a maize line of deficient in starch biosynthesis, transformed with a gene encoding a cell glucan is produced in the amyloplast and/or vacuole or a maize line of glucosyltransferase B or D enzyme, wild-type or mutant and a paper of producing a glucan (paper sizing/coating agent). The vector is useful comprising the glucan in a plant. The method comprises transforming a cell with the vector, growing the plant cell under plant growing conditions to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the cregenerated plant, where the vector contains a transit sequence from cell produced in the amyloplast of potato or the vacuole of sugar beet. Cell company is a substitutes for and additions to modified starch cell cand latexes in paper manufacture. Unlike prior art techniques, which cell interest input materials that produced by GTP, which utilises biologically produced input materials, is more cost-effective and cell properties and impart gloss to the paper during coating the present sequence is not shown in the specification but was created by the indexer casing the GTPB sequence appearing as AAU98027 and the information in
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector, a seed or tuber from the transgenic plant, a paper sizing amm/ou coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, thermoplastic molecule or their combinations or glucan and starch where thermoplastic molecule or their combinations or glucan and starch where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1475
16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                     Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                    S. mutans glucosyltransferase GTFB mutant K779Q.
                                                                                                                                                                                                                                                                                                                       Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU98040 standard; protein; 1475 AA
                                                                                                                                                                     14-MAR-2002
                                                                                                                                                                                                    US2002031826-A1
                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                       Synthetic.
                                               16-JAN-1998;
                                                               07-JUN-1995
                                                                                07-JUN-1995;
                                                                                                  07-JUN-1995;
                                                                                                                                  19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPNYVFIRAHDSEVQTRIAKII 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                     2000US-00740274.
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95US-00478704.
95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                      /note= "Wild-type Lys substituted by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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Pred. No.
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5.6e-05;
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Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in paper manufacture, comprises mutations in specific positions.
                                                                                                                                                                         Claim 36; Page; 44pp; English
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CC complementary polymucleotide, a ribonucleic acid sequence encoding the CC linked to a promoter, a vector comprising the polymucleotide operably CC linked to a promoter, a vector comprising the expression cassette, host CC cell introduced with the vector, a transgenic plant, a paper sizing and/or vector, a seed or tuber from the transgenic plant, a paper sizing and/or CC oating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTF, will type or, starch, a latex, and the applicability of the modifications or glucan and starch where CC deficient in starch biosynthesis, transformed with a gene encoding a glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC comprising the glucan in a plant. The method comprises transforming a glucosyltransferase B or D enzyme, wild-type or mutant and apaper CC plant cell with the vector, growing the plant cell under plant growing CC conditions to produce a regenerated plant and inducing expression of the polymucleotide for a time sufficient to produce the glucan in the crimal cc ribulose biphosphate carboxylase small subunit, waxy, brittle-I and CC composition the amyloplast of potato or the vacuole of sugar beet. CC glucans are useful as substitutes for and additions to modified starch cC and latexes in paper manufacture. Unlike prior art techniques, which cc require input materials that produce begins a fluents, paper CC conjuctably produced input materials, is more cost-effective and cc plants and impart gloss to the paper during step. The present sequence is not shown in the specification but was created by the indexer using the GTPB metant of the invention. Note: The present cc lasing the GTPB metant of the invention. Note: The present consists of the invention but was created by the indexer classing the sequence appearing as AAU98027 and the information in The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K/K1014T, T169A/Y17DA/Y17DA, and K779Q or a I448V/D457N/D567T/D571K/K779Q/K1014T, Y169A/Y17DA/Y17DA, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D, N471D/T589D, and N471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polymucleotide which encodes P1 or P2, or its complementary polymucleotide, a ribonucleic acid sequence encoding the grap mutant an avaraged an areast a communication the complementary polymucleotide, a ribonucleic acid sequence encoding the

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                                                                                                                                                                                                                            Sequence 1475 AA;
         S. mutans glucosyltransferase GTFB mutant K1014T
                                   27-AUG-2002 (first entry)
                                                                              AAU98033 standard; protein; 1475 AA
                                                                                                                                                           1 VPNYVFIRAHDSEVQTRIAKII 22
                                                                                                                                     VPSYSFIRAHDSEVQDLIADII 573
                                                                                                                                                                                 Conservative
                                                                                                                                                                                             72.7%;
77.3%;
                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                             Score 80;
Pred. No.
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The invention an isolated protein comprising a glucosyltransferase (GTF) CC K1014T, D457N/D567T, D457N/D571K, D567T/D571K, M57N/D57TK, D567T/D57TK, M567T/D57TK, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in paper manufacture, comprises mutations in specific positions.
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                                                                                                                                           GTFB sequence appearing as AAU98027 and
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hypothetical prote in BR protein - Str virulence-associat plasma hyaluronan-hypothetical prote hypothetical prote probable pyruvate decarboxy aspartyl-trana synt probable pyruvate hypothetical prote hypothetical prote genome polyprotein B hom hypothetical prote sigma NS protein - unp-N-acetylglucos hypothetical prote flagella-associate sigma NS protein - hypothetical prote eleghemoglobin - galdehyde dehydroge HCRF3 protein hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote aspartyl-tRNA synt aspartate-tRNA lighypothetical prote aspartyl-tRNA synt adapter protein - genome polyprotein - sigma NS protein - sigma NS protein - sigma NS protein - sigma NS protein hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical protein translation activa sigma NS protein - sigma NS protein - sigma NS protein hypothetical prote hypoth

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ALIGNMENTS

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dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans C,Species: Streptococcus mutans C,Species: Streptococcus mutans C,Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 C;Accession: A45866 R;Honda, O.; Kato, C.; Kuramitsu, H.K.
J. Gen. Microbiol. 136, 2099-2105, 1990
A;Title: Nucleotide sequence of the Streptococcus mutans gtfD gene encoding the glucosyl A;Reference number: A45866; MUID:9110095B; PMID:2148600
A;Accession: A45866
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A;Title: Analysis of the Streptococcus downei gtfS gene,
A;Reference number: A41483; MUID:90316665; PMID:2142479
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A; Residues: 1-1365 <GIL>
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probable dextransucrase (EC 2.4.1.5), extracellular - Leuconostc (Species: Leuconostcoc mesenteroides C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change C; Accession: T31098
R; Monchois, V.; Remaud-Simeon, M.; Monsan, P.; Willemot, R.M.
                                                                                                                              T31098
                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1127-1146/Domain: cpl repeat homology <CP2>
F;1192-1211/Domain: cpl repeat homology <CP3>
F;1192-1211/Domain: cpl repeat homology <CP4>
F;1257-1276/Domain: cpl repeat homology <CP5>
F;1277-1297/Domain: cpl repeat homology <CP5>
F;1321-1340/Domain: cpl repeat homology <CP6>
F;1341-1361/Domain: cpl repeat homology <CP6>
F;1385-1404/Domain: cpl repeat homology <CP7>
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A,MOLecule type: DNA
A,MOLecule type: DNA
A,Residues: 1-1431 <HON>
A;Cross-references: GB:M29296
A;Cross-references: GB:M29296
C,Superfamily: cpl repeat homology
C,Superfamily: cpl repeat homology
F;181-201/Domain: cpl repeat homology
F;181-201/Domain: cpl repeat homology
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100.0%; Pred. No. 1.2e-09;
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90.0%;
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Pred. No. 2.5e-06;
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A;Residues: 1-1508 <MON>
A;Cross-references: EMBL:AF030129;
A;Experimental source: strain NRRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
JC5473
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A;Description: produces dextran composed only of alpha(1-6) glucosidic bonds
C;Keywords: glycosyltransferase; hexosyltransferase
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A;Title: Cloning and sequencing of a gene coding for a novel
A;Reference number: JC5473; MUID:97136886; PMID:8982063
A;Accession: JC5473
A;Status: nucleic acid sequence not shown; translation not sh
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R;Monchois, V; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R;Monchois, V.; Willemot, R
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C;Species: Leuconostoc mesenteroides
C;Date: 07-011-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
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A;Gene: dsrB
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C; Genetics:
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A;Cross-references: GB:U38181
C;Comment: This enzyme catalyzes the transfer of D-glucopyranosyl
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                                                                                                                                                                                                                                C;Accession: B33135; A33128
R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4270, 1987
A;Title: Sequence analysis of the gtfB gene from Streptococcus
A;Reference number: A33135; MUID:87308013; PMID:3040685
A;Accession: B33135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: glycosyltransferase; hexosyltransferase F;78-870/Domain: catalytic #status predicted <CAT> F;922-1290/Domain: glucan-binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Streptococcus mutans
C;Date: 23-Oct_1990 #sequence_revision 23-Oct-1990 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtfB protein precursor - Streptococcus mutans
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               A;Cross-references: GB:M17361; NID:g153639; PIDN:AAA88588.1; R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K. submitted to the Protein Sequence Database, September 1990
                                                                                                                             A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1475 <SHI>
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1 Similarity 77.3%;
17; Conservative
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85.7%;
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Pred. No. 2.7e
3; Mismatches
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Pred. No.
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B-1299
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hes 2;
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A; Experimental source: strain GS-5
C; Superfamily: cpl repeat homology
F;1096-1115/Domain: cpl repeat homol
F;1224-1243/Domain: cpl repeat homol
F;1289-1308/Domain: cpl repeat homol
F;1354-1373/Domain: cpl repeat homol
F;1354-1394/Domain: cpl repeat homol
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A; Residues: 1-171,173-641,'N',643-1475 <SH2>
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A;Status: preliminary; not compared with conceptual translation
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C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Streptococcus salivarius ATCC 25975 possesses at A;Reference number: Z20909; MUID:95122197; PMID:7822030 A;Accession: T30858
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                                                                        A;Molecule type: DNA
A;Residues: 1-1375 <UED>
A;Experimental source: GS-5
R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
T. Bacteriol. 169, 4263-4270, 1987
J. Bacteriol. 169, 4263-4270, 1987
A;Title: Sequence analysis of the gtfB gene from Streptococcus mutans.
A;Reference number: A33135; MUID:87308013; PMID:3040685
A;Recession: C33135
A;Accession: C33135
A;Status: preliminary
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A,Cross-references: EMBL:L35928; NID:g662380; PID:g662381; PIDN:AAC41413.1
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                                                                                                                                                                                                                                                              C;Accession: JT0345; C33135
R;Ueda, S.; Shiroza, T.; Kuramitsu, H.K.
R;Ueda, S.; Shiroza, T.; Kuramitsu, H.K.
R;Ueda, S.; Shiroza, T.; Kuramitsu, H.K.
R;Ueda, S.; Shiroza, T.; Kuramitsu, H.K.
Refere from Strepto
A;Reference number: JT0345; MUID:89137980; PMID:2976010
A;Accession: JT0345
                                                                                                                                                                                                                                                                                                                                                                                                                         dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans (strain GS-5) N,Alternate names: sucrose 6-glucosyltransferase
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
A; Residues: 1-349
A; Cross-references
C; Genetics:
                                                         A; Molecule type: DNA
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Best Local 9
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        Cross-references: GB:
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ilarity 77.3%;
Conservative
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; Pred. No. 0.00
3; Mismatches
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Pred. No. 0.00
1; Mismatches
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C;Keywords: duplication; glycosyltransferase; hexosyltransferase;;1-34/Domain: signal sequence #status predicted <SIO> F;35-1375/Product: glucosytransferase #status predicted <MAT> F;1126-1145/Domain: cpl repeat homology <CP1> F;1253-1272/Domain: cpl repeat homology <CP2> F;1318-1337/Domain: cpl repeat homology <CP3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: ATCC 25975

R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A.
J. Gen. Microbiol. 137, 2577-2593, 1991

A;Title: Molecular characterization of a cluster of at least two glucosyltransferase A;Reference number: A44811; MUID:92148377; PMID:1838391

A;Accession: S28810
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A; Accession: $22737
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                                                                                                                                                                                                                                                                                                       RESULT 9
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A;Cross-references: EMBL:Z11872; NID:g47530; PIDN:CAA77898.1; PID:g47531
                                                                                                                                                                                                              glucosyltransferase - Streptococcus salivarius
C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
C;Accession: T30857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: gtfK
C;Superfamily: cpl repeat homology
C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;1456-1475/Domain: cpl repeat homology <CPR>
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A; Residues: 1-51 <GIF>
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                                    A;Accession: T30857
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1449 <81M>
                                                                                                                          R;Simpson, C.L.; Giffard, P.M.; Jacques, N.A.
Infect. Immun. 63, 609-621, 1995
A;Title: Streptococcus salivarius ATCC 25975 possesses at A;Reference number: Z20909; MUID:95122197; PMID:7822030
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Function:
A;Cross-references:
C;Genetics:
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Best Local
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                      EMBL:L35495; NID:g662378; PID:g662379; PIDN:AAC41412.1
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72.7%;
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Pred. No.
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Pred. No. 0.00088;
2; Mismatches 2
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0.00051
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glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius C;Species: Streptococcus salivarius C;Species: Streptococcus salivarius C;Decies: Streptococcus salivarius C;Decies: Streptococcus salivarius C;Decies: A44811; S23726; S28809 R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A. J. Gen. Microbiol. 137, 2577-2593, 1991 A;Title: Molecular characterization of a cluster of at least two A;Beference number: A44811; MUID:92148377; pMID:1838391 A;Accession: A44811
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C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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A; Accession: T30552
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A; Cross-references: EMBL: Z11873; NID: 947526; PIDN: CAA77900.1;
A; Cross-references: EMBL: Z11873; NID: 947526; PIDN: CAA77900.1;
A; Cross-references: EMBL: Z11873; NID: 947526; PIDN: CAA77900.1;
A; Cross-references: EMBL: Z11873; NID: 947526; PIDN: CAA77900.1;
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A; Cross-references: EMBL: Z11873; NID: 947526; PIDN: CAA77900.1;
A; Cross-references: EMBL: Z11873; PIDN: CAA77900.1;
A; Cross-references: EMBL: Z11874; PIDN: CAA77900.1;
A; Cross-references: EMBL: Z11874; PIDN: CAA77900.1;
A; Cross-refer
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RESULT 12
A38175
Glucosyltransferase precursor - Streptococcus sobrinus
Glucosyltransferase precursor - Streptococcus sobrinus
C;Species: Streptococcus sobrinus
C;Species: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 15-Oct-1999
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 15-Oct-1999
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70.0%;
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 Mismatches

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Pred. No. (
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Pred. No.
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Pred. No. 0.0018;
2; Mismatches
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NCBIP:81052)
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J. Bacteriol. 173, 989-996, 1991
A;Title: Peptide sequences for sucrose splitting and glucan binding within Streptococcus A;Reference number: A38175; MUID:91123227; PMID:1704006
A;Status: preliminary
A;Molecule type. Par
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A;Residues: 1-1592 <ABO>
A;Cross-references: GB:D90213; NID:g217032; PIDN:BAA14241.1;
C;Superfamily: cpl repeat homology
E;1093-1112/bomain: cpl repeat homology <CP1>
F;1222-1241/Domain: cpl repeat homology <CP2>
F;1287-1306/Domain: cpl repeat homology <CP3>
F;1330-1351/Domain: cpl repeat homology <CP4>
F;1352-1371/Domain: cpl repeat homology <CP5>
F;1462-1420/Domain: cpl repeat homology <CP5>
F;1462-1420/Domain: cpl repeat homology <CP6>
F;1463-1532/Domain: cpl repeat homology <CP7>
F;1513-1532/Domain: cpl repeat homology <CP8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aspartate-tRNA ligase (EC 6.1.1.12) - syphilis spirochete N;Alternate names: aspartyl-tRNA synthetase TP0985 C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24_Jul-1998 #sequence_revision 24-Jul-1998 #text_change 03-Jun-2002
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                                                                                                                                                            A,Pathway: protein biosynthesis
C;Superfamily: lysine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                    A;Residues: 1-602 <COL>
A;Cross-references: GB:AE001266; GB:AE000520; NID:g3323309; PIDN:AAC65942.1; PID:g332331
A;Experimental source: strain Nichols
C;Genetics:
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                                                                                                                                                                                                                                              A;Gene: TP0985
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Complete genome sequence of Treponema pallidum, A; Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                    A; Description: activates amino acid and transfers
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9; Conserva
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sugar kinase, FGGY family - Thermotoga maritima (strain MSB8)
C,Species: Thermotoga maritima
C,Species: Thermotoga maritima
C,Date: 11-Jun-1999 #text_change 21-Jul-2000
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C,Accession: C72417
R,Melson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
R,Melson, K.E.; Clayton, R.A.; Gotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ri
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ri

Richardson,

Hicke

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Nature 399, 323-329, 1999
A;Tille: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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A;Experimental source: strain MSB8
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A; Residues: 1-492 < ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: aspartyl-tRNA synthetase
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
C;Date: 15-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
C;Accession: E70155
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                                                                                                                                                    R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma A;Reference number: $73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-506 <KLE>
A;Residues: 1-506 <KLE>
A;Cross-references: GB;AE001149; GB:AE000783; NID:g2688348; PIDN:AAB91506.1; PID:g268834
A;Experimental source: strain B31
C;Superfamily: lysine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
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N;Alternate names: aspartyl-tRNA synthetase aspS; hypothetical protein D09_orf557
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                                                 A; Molecule type: DNA
A; Residues: 1-557 < HIM>
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                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Cross-references: EMBL:AE000013; GB:U00089; NID:g1673762; PIDN:AAB95756.1; PID:g167376
Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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A87374
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                                         A;Cross-references: EMBL:Z34098; NID:g496934; PIDN:CAA84002.1; A;Note: the nucleotide sequence was submitted to the EMBL Data R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, September 1995 A;Reference number: S56835
                                                                                                                                                                    A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-654 <\VAN>
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A; Residues: 1-654 < DIE>
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: A87374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: aspS
A;Gene: code: SGC3
A;Genetic code: SGC3
C;Superfamily: lysine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005673; NID:gl3422293; PIDN:AAK22989.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-498 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein CC1005 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: A87374
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text_change 12-Nov-1999
C;Accession: S05829; S50776; S56999; S56996; S45164
R;Dieckmann, C.L.; Homison, G.; Tzagoloff, A.
J. Biol. Chem. 259, 4732-4738, 1994
A;Title: Assembly of the mitochondrial membrane system. Nucleotide sequence A,Title: Assembly of the mitochondrial membrane system. Nucleotide sequence A,Reference number: S05829; MUID:84185566; PMID:6325407
A;Accession: S05829
                                                                                                                                                                                               CBP1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein HRA654; protein JU242; protein YJL209w
                                                                                                                                                                                                                                                                          RESULT 18
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Best Local Similarity
                                                                                                                                                                      Species: Saccharomyces cerevisiae
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75.0%;
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Pred. No.
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Pred. No.
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                                                              Nucleotide sequence of
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                                                                      a yeast
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PID:g496953 Library, June 1994

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nine-cis-epoxycarotenoid dioxygenase homolog F28J12.10 - Arabidopsis thaliana N;Alternate names: hypothetical protein T9A21.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T04531; T04937
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; submitted to the Protein Sequence Database, February 1998
A;Reference number: Z15377
A,Accession: T04531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z49484; NID:g1015590; PIDN:CAAB9506.1; PID:g1015591; GSPDB:GNO.R;Purnelle, B.; Coster, F.; Goffeau, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 637-654 < PUR>
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A; Residues: 1-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Experimental source: cultivar Columbia; BAC clone F28J12 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, submitted to the Protein Sequence Database, February 1999 A;Reference number: Z15390 A;Accession: T04937
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conserved hypothetical protein MYPU_7040 [imported] - Mycoplasma pulmonis (.C;Species: Mycoplasma pulmonis (.pate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: H90599
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.
                                                                                             RESULT 20
H90599
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL021713
A;Experimental source: cultivar C
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A; Residues: 1-377 <B
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A;Cross-references: EMBL:AL021710
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A; Residues: 1-583 <BEV>
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9; Conserva
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42.1%;
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Pred.
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29;
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         V.; Samson, D.; Galisson, F.;
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    Mycoplasma pulmonis (strain UAB

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A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: H90599
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A;Genetic code: SGC3
C;Superfamily: conserved hypothetical protein MG139
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                                                                                                                                                                                                                                                                                                                                               Ristephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, K.; Alaying, H.; Piccines, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: H71553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable biotin carboxylase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
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A;Experimental source: strain UAB CTIP
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A; Residues: 1-631 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                         A;Cross-references: GB:AE001286; GB:AE001273; NID:g3328516; PIDN:AAC67715.1; PID:g332852
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-457 < ARN>
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                                                                                                                                                              C;Superfamily: 1 F;3-448/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                Superfamily: biotin carboxylase; biotin carboxylase homology 3-448/Domain: biotin carboxylase homology <BCH>
                                                                                                                                                                                                     Gene: accC
                                                                             Matches
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                                                                                                   Local
219 NYVYLGERDCTVORRROKLI
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                                      3 NYVFIRAHDSEVQTRIAKII
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45.0%;
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                                                                                                       Pred. No.
                                                                                                                           Score 43;
      238
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                                                                                    Mismatches
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G. Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumo A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: D81708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetyl-coenzyme A carboxylase, biotin carboxylase TC0400 [imported] - Chlam C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
A; Gene: TC0400
C; Superfamily:
                                                                   C; Genetics:
                                                                                                  A,Cross-references: GB:AE002306; GB:AE002160;
A,Experimental source: strain Nigg (MoPn)
                                                                                                                                                                   A; Residues: 1-457 <TET>
                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: D81708
                                        TC0400
      biotin carboxylase; biotin carboxylase homology
                                                                                                                                       NID: 97190428; PIDN: AAF39257.1;
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0.; Hickey,

PID:g71904

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RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein - Symechocystis sp. (strain PCC 6803)
C;Species: Symechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S75712
C;Accession: S75712
S; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; leader, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, T.; Watanabe, A.; Yamada, T.; Sequence analysis of the genome of the unicellular cyanobacterium A; Title: Sequence analysis of the genome of the unicellular cyanobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-765 < KAN>
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A;Accession: S76795
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A;Residues: 1-1070 < KAN>
A;Cross-references: EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA10447.1;
A;Cross-references: EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA10447.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June C;Superfamily: bacterial cellulose-binding domain homology <BCB1>
F;7-112/Domain: bacterial cellulose-binding domain homology <BCB2>
F;7-112/Domain: bacterial cellulose-binding domain homology <BCB2>
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Similarity 45.0%;
9; Conservative
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4; Mismatches
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; protein slr0897
                                                                                                                                                       1.1e+02
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to the EMBL Data Library, June 1996
                                                                                                                                                                          DB 2;
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Yamada, M.; Ya
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A,Accession: H83933
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A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB05991.1; A;Experimental source: strain C-125 C;Genetics:
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                                                                     A; Molecule type: DNA
A; Residues: 1-144 <STO>
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27

haloduran

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GSPDB:GN00

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R;Delorme, C.; Ehrlich, S.D.; Renault, P.
J. Bacteriol. 174, 6571-6579, 1992
A;Title: Histidine biosynthesis genes in Lactococcus lactis A;Reference number: A45734; MUID:93015709; PMID:1400209
A;Reference R5002118
A;Accession: E47754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yceA protein homolog (3' to hisIE) - Lactococcus lactis subsp. lactis (fragment) C;Species: Lactococcus lactis subsp. lactis
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                                                                                                                                            A;Gene:
C;Superf
                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein ymdE [imported] - Lactococcus lactis subsp. lactis (strain C,Species: Lactococcus lactis subsp. lactis c,Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C,Accession: A86777
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A; Residues: 1-92 <DEL>
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A86777
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A;Cross-references: GB:AE005176; PID:G12724186; PIDN:AAK05315.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                     R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001
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PNNRYIKAHQLSNQEVQERLA 311
                                     PNYVFIRAH---DSEVOTRIA 19
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Pred. No. 7.
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Pred. No. 3
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A;Gene: BH2272

Query Match

Local

38.2%;

Score 42; DB Pred. No. 16;

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Length 144;

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N;Alternate
C;Species M
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A;Genetic code: SGC3
C;Superfamily: transcription elongation factor
C;Keywords: transcription factor
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                                                                                                                                                                                                                                          A;Cross-references: EMBL:AE000043; GB:U00089; NID:g1674122; PIDN:AAB96085.1; PID:g167412
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription elongation factor greA - Mycoplasma pneumoniae (strain NyAlternate names: hypothetical protein F11_orf160
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A; Residues: 1-346 < COL>
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A;Accession: E70715
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C;Species: Mycobacterium tuberculosis
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Matches 8
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;Residues: 1-160 <HIM>
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                                                                                                                  Query Match
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Similarity 50.0%;
8; Conservation
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Search completed: May Job time : 14.6667 sec

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C;Superfamily: transcription elongation factor greb
C;Keywords: transcription factor
                                                                                                                                                                                                                                                                                                                                                                C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7563993
            片
                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-161 < TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.I. M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
B64231
                                                                                                                                                                                                                                                      A; Cross-references: GB:U39708;
A; Experimental source: strain G
                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription elongation factor greA homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #8equence_revision 17-Nov-1995 #text_change 21-Jul-2000
C;Accession: B6423
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                                           3 NYVFIRAHDSEVQTRIAKI
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ALIGNMENTS

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InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01473; CM binding 1; 8.
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                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: Belongs to family 70 of glycos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glimore K.S., Russell R.R., Ferretti J.J.;
"Analysis of the Streptococcus downei gtfS gene, which
glucosyltransferase that synthesizes soluble glucans.";
Infect. Immun. 58:2452-2458(1990).
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Gilmore K.S., Russell R.R., Ferretti J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilmore K.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus downei (Streptococcus sobrinus).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-S precursor (EC 2.4.1.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Sucrose + {(1,6) alpha-D-glucosyl}(N) = D-fructose + {(1,6) -alpha-D-glucosyl}(N+1).

ENZYME REGULATION: GLUCAN SYNTHESIS BY GTF-S IS INDEPENDENT OF PRIMER GLUCAN UNLIKE GTF-I.

MISCELLANEOUS: GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA
    537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND ME AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
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RESULT

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EMBL; M29296; AAA26895.1; --
EMBL; D88653; BAA26103.1; --
EMBL; D88656; BAA26107.1; --
EMBL; D88659; BAA26111.1; --
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EMBL; D88659; BAA26111.1; --
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between the Swiss Institute of Bioinformatics and the EMBL
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STRAIN=MT4239 / Serotype C, MT4245 /
MT4467 / Serotype E, and MT8148 / Ser
MEDLINE=98231643; PubMed=9570124;
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Honda O., Kato C., Kuramitsu H.K.;
"Nucleotide sequence of the Streptococcus
the glucosyltransferase-S enzyme.";
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GTFD OR SMU.910.
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FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECOME THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGREGATION OF HACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: Sucrose + { (1,6)-alpha-D-glucosyl} (N) = D-frictose + { (1,6)-alpha-D-gl
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SIMILARITY: Contains 6 cell wall binding repeats.
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IPR002479; CW_binding.
IPR003318; Glyco_hydro_70.
l473; CW_binding_1; 11.
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EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
THE DENTAL PLAQUE BECA
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erotype C;
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G -> R (IN STRAIN MT425).

H -> Q (IN STRAIN MT4239).

Y -> C (IN STRAIN MT4239).

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K -> T (IN STRAIN MT4245).

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R YYDKNSGNMYNKVUTLANGRRIGIDRWGIARYY ->

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STRALI=MT4239 / Serotype C, MT4245
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MEDLINE=98231643; PubMed=9570124;
Pujiwara T., Terao Y., Hoshino T.,
Kimura S., Hamada S.;
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MEDLINE=87308013; PubMed=3040685;
chirora T.. Ueda S., Kuramitsu H.K.;
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Li S., Zhu H.,
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STRAIN=UA159 / ATC
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Ueda S., Shiroza T., Kuramitsu H.K.;
"Sequence analysis of the gtfC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-349 FROM N.A.
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SIMILARITY: Belongs to family 70
SIMILARITY: Contains 5 cell wall
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NTCE TRACT 700610 / Serotype C;
NE=21295063; PubMed=12397186;
D., McShan W.M., McLaughlin R.E., Savic G., Cham M.B., Primeaux C., Tian R., Kenton S., Jia H., Zhu H., Najar F., Lai H., White J., Roe B.A., The Requence of Streptococcus mutans UA159, a car
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                                                                                                     equires a email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 09, Createq, (Rel. 41, Last sequence update) (Rel. 42, Last annotation update) (Rel. 42, Last annotation (BC 2.4.1.5)
; AAA88592.1;
; BAA26102.1;
; BAA26106.1;
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license@isb-sib.ch)
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V -> I (IN STRAIN MT8148).
D -> N (IN STRAIN MT4239).
V -> I (IN STRAIN MT4239).
V -> I (IN STRAIN MT4239 AND MT8148).
S -> P (IN STRAIN MT6148).
GRIPFKSNGVOAKGELITERKGRIKYTDPNSGNEVRNRYVR
TSSGNMYYFGNDGYALIGMHVVEGRRVYFENGGVRYYRASHD
QRNHMDYDTRDDFGRGSSSAVRFHSRNGFFNNFFRF ->
HASILSLMVFRLRESSLQSVKVVSNTMILIFEMKFVIVM
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MISSING (IN STRAIN MT8148).

I -> V (IN STRAIN MT8148).

T -> A (IN STRAINS GS-5, MT42
AND MT8148).

R -> K (IN STRAIN MT8148).

V -> I (IN STRAIN MT8148).

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IN STRAIN MT4251).

IN STRAINS MT4245 AND MT4251).

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RESULT

InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PP01473; CW_binding_1; 7.

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EMBL; M17361; AAA88588.1; -. EMBL; D88651; BAA26101.1; -. EMBL; D88654; BAA26109.1; -. EMBL; D88657; BAA26119.1; -. EMBL; D88657; BAA26119.1; -. EMBL; D89977; BAA26119.1; -. EMBL; AB014940; AAN85705.1; -. PIK; B33135, B33135.
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01-NOV-1988 (Rel. 09, Created)
28-FEB-2003 (Rel. 41, Last sequen
10-OCT-2003 (Rel. 42, Last annota
Glucosyltransferase-I precursor (
(Successe 6-glucosyltransferase).
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STRAIN=UA159 / ATCC 700610 / Serotype
TNR=22295063; PubMed=12397186;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MT4339 / Serotype C, MT4245 /
MT4467 / Serotype B, and MT8148 / Se;
MEDLINE=98231643; PubMed=9570124;
Finitiwara T., Terao Y., Hoshino T., K
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Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
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SIMILARITY: Contains 10 cell wall binding
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CATALYTIC ACTIVITY: SUCTOSE + { (1,6)-alpha-D-glucosyl} (N)

fructose + { (1,6)-alpha-D-glucosyl} (N+1).

SUBCELLULAR IOCATION: Secreted.

MISCELLANBOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS

1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESII

WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESII

WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUTERING ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
552
                                                                                                                                                                                                                                                                                                                                                                                                                                        PF02324; Glyco_hydro_70; 1.
ferase; Glycosyltransferase; Signal; Repeat; Dental caries;
            μ
                                Similarity
            VPNYVFIRAHDSEVQTRIAKII 22
VPSYSFIRAHDSEVQDLIRDII 573
                                                                                                                                                                                                                                                                                                                                                                                                                                     proteome.
                                                  1310
1476
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1097
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11225
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1290
1355
                         Conservative
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474
512
519
701
708
938
952
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570
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276
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                                                   165846
                                                   MW;
                         1;
                        Score 75; DB
Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                   F -> L (IN
FGKPVE -> Y:
AND MT4467)
SV -> NT (II
MT4467)
ADS -> VDG
MT4467)
                                                                                        AND MT8148)
S -> G (IN
AND MT8148)
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S -> G (IN AND MT8148)
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В -> А
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N -> R
I -> T
K -> R
F -> Y
T -> I
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T -> I
V -> A
MT4467
Q -> P
I -> S
I -> F
S -> F
K -> N
S -> P
                                                                                                                                             ADQDVRVAASTAPSTDGK -> LIKMFALRLARPHQQMA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE)
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                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
X TAND
                                                  9C6E09F731B4CBCF
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                                                                                                                                        T (IN STRAIN MT4239).

(IN STRAIN MT4239).

Y (IN STRAIN MT4251).

K (IN STRAIN MT8148).

C (IN STRAIN MT8148).

P (IN STRAIN MT4239).

P (IN STRAIN MT4239).

H (IN STRAIN MT8148).

H (IN STRAINS GS-5 AND
H (IN STRAINS GS-5, MT4
TRAIAS)
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                                                                             (IN REF.
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N STRAIN MT4251).
N STRAINS GS-5, N
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D MT8148).
D STRAIN MT4251).
N STRAINS GS-5, M
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STRAIN
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                                      DB 1;
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STRAIN GS-5).
                                                         REF.
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                                .00042;
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                                     Length 1476;
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WT4239)
WT8148)
WT8148)
WT8148)
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WT8148)
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                                                  CRC64;
                         Indels
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5, MT4239, MT
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                                                                                                          AND MT4467)
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RESULT 5
GTF1_STRDO

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                                               Query Match
Best Local S
Matches 15
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P11001;
01-JUL-1989
01-JUL-1989
10-OCT-2003
                                                                                                                            SIGNAL
CHAIN
DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
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REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                       InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 70.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01473; CW binding 1; 16.
Pfam; PF02324; Glyco hydro 70; 1.
Transferase; Glycosyltransferase; Signal; Repeat; Dental caries.
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M17391; AAC63063.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol.
-!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus.
NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus downei (Streptococcus sobrinus).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Sucrose 6-glucosyltransferase) GTFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of a glucosyltransferase sobrinus MFe28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87309014; PubMed=3040686;
Perretti J.J., Gilpin M.L., Russell R.R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THO TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAÇUE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE T AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = fructose + {(1,6)-alpha-D-glucosyl}(N+1).

SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to family 70 of glycosyl hydrolases. SIMILARITY: Contains 19 cell wall binding repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANBOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE G
1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI
FORMS OF GLUCANS.
554 VPSYSFARAHDSEVQDLIRDII 575
                                               15; Conservative
                     VPNYVFIRAHDSEVQTRIAKII
                                                                                                                                        1099
1099
1099
1163
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1292
1352
1406
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                                                                                                   177080
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AC REPEAT.
AC REPEAT.
B REPEAT.
B REPEAT.
B REPEAT.
B REPEAT.
AC REPEAT.
AC REPEAT.
AC REPEAT.
                                              Score 70; DB
Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                                   1.25 A, 2
A REPEAT.
                                                                                                                                                                                                                               CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE)
1.25 A, 2 B, AND 5 AC REPEAT
                                                                                                                                                                                                                                                                        GLUCOSYLTRANSFERASE-I
                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                                                   B9E86A200868798E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1597
                                                                                                                                                                                                                                                                                                                                                                                                    noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                         DB 1;
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                                                 6
                                                                        Length 1597;
                                                 Indels
                                                                                                   CRC64;
                                                                                                                                                                                                                                  REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E GLUCANS (ALPH
S SYNTHESIZES
SI SYNTHESIZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Dextransucrase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
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В
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GTF2_STRDO
                                                                                          Matches
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Best Local
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01-AUG-1992 (Rel. 23, 01-AUG-1992 (Rel. 23, 101-OCT-2003 (Rel. 42, 101-OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBI, D90213; BAA14241...,
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro 70.
InterPro; CW binding I; 13.
InterPro; PP01473; CW binding I; 13.
In Proceeding I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-!- CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = D-fructose + {(1,6)-alpha-D-glucosyl}(N+1).

-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANBOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOOKED AND SOME 1,6-GLUCOSE).
                                                                                                                                                                                                                                                    REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-6715 / Serotype G;
MEDLINE=91123227; PubMed=1704006;
Abo H., Matsumura T., Kodama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus.
NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Sucrose 6-glucosyltransferase).
Streptococcus downei (Streptococcus sobrinus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Last annotation update) Glucosyltransferase-I precursor (EC 2.4.1.5)
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetase).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kagawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 173:989-996(1991).

- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUSE TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to family 70 of glycosyl hydrolases. SIMILARITY: Contains 16 cell wall binding repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORMS OF GLUCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRDO
                                                                                        Similarity
15; Conserv
  VPSYSFARAHDSEVQDIIRDII
                                             VPNYVFIRAHDSEVQTRIAKII
                                                                                                                                                                                   1093
1093
1093
1158
1122
1227
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1402
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                                                                                          Conservative
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1592
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1592
1044
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11492
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1207
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1272
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                                                                                                           62.7%;
                                                                                                                                                                                 176167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transferase; Signal; Repeat; Dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                                                                                                                                 MW.
                                                                                   Score 69; DB 1;
Pred. No. 0.0044;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
6.5 x TANDEM REPEATS.
                                                                                                                                                                                 (INCOMPLETE).
BC0A66D079351ECF CRC64;
  569
                                             22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GTF-I) (Dextransucrase)
                                                                                        6,
                                                                                                                                   Length 1592;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THAT ARE THOUGHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                                                      <u>.,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outstation
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SYDUTE
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ID ACCORDANCE
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InterPro; IPR004524; AspS bact.
InterPro; IPR004524; ASD dom.
InterPro; IPR004115; GAD dom.
InterPro; IPR004994; Nucleic_acid_OB.
InterPro; IPR004364; tRNA-synt_2.
InterPro; IPR004365; tRNA-synt_asp.
InterPro; IPR004365; tRNA_nit;
InterPro; IPR006195; tRNA_ligase_II.
pfam; pf02398; GAD; 1.
pfam; pf00152; tRNA_synt_2; 2.
pfam; pf01336; tRNA_anti; 1.
printerPro; PR01042; TRNASYNTHASP.
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15-DEC-1998
28-FEB-2003
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PIR; A71256; A71256.
HSSP; P36419; 1EFW.
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O83950;
                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                            Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO0459; aspS bact; 1.
PROSITE; PS50862; AA TRNA LIGASE II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
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-i- SUBUNIT: Homodimer (By similarity).
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Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASPS OR TP0985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98332770; PubMed=9665876;
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                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                                                                                                  Similarity 9; Conserv
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602 AA;
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Last sequence update)
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ase (EC 6.1.1.12) (Aspartate--tRNA ligase)
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                                              22
                                                                                                                                                                                                                                                         Protein biosynthesis; Ligase;
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                                                                                                                              Pred.
                                                                                                                                                    Score 49;
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RA Addmen M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addmen M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Addmen M.D., Celniker S.E., Holt R.A., Howeling R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Hallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Horkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Horkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Horkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Geolee C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.I., Harvey D.A., Heiman T.J., Herrandez J.R., Houck J.,
RA Harris N.I., Harvey D.A., Heiman T.J., Hermandez J.R., Houck J.,
RA Harris N.I., Harvey D.A., Reiman T.J., Hermandez J.R., Houck J.,
RA Harris N.I., Harvey D.A., Reiman T.J., Hermandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.I., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lini X.,
Iti X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Musskern D.R., Sende M.G.,
RA Shue B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
RA Shenga X.H., Kanga T.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shenga R.A., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Shenga R.A.
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RA51_DROM
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Q27297; Q9VAA8;
Q1-NOV-1997 (Re.
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10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-NA repair protein Rad51 homolog (RecA protein homolog).
RAD51 OR DMR OR CG7948.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Rukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCKee B.D., Ren X.J., Hong C.S.;

"A recA-like gene in Drosophila melanogaster that is expressed high levels in female but not male meiotic tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Oregon-R;
MEDLINE=96207535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akaboshi E., Inoue Y., Ryo H.; "Cloning of the cDNA and genomic DNA that correspond to the recA-like gene of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95161094; PubMed=7857671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Canton-S
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FUNCTION: Binds to single and double stranded DNA and exhibits
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                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
SECUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE-97105885; PubMed=8948633;
MEDLINE-971ch R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
01-NOV-1997
28-FEB-2003
between the Swiss Institute of Bioinformatics Institute. The Buropean Bioinformatics Institutions as long
                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation -
                                                                                                                                                                                               SYD_MYCPN
P75068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50162; RECA 2; 1.

PROSITE; PS50163; RECA 3; 1.

DNA-binding; ATP-binding; Nuclear .

NP BIND 124 131 ATP (
SEQUENCE 336 AA; 36647 MW; P9E
                                                                                                                                      diphosphate + L-asparty1-tRNA(Asp).
-I- SUBUNIT: Homodimer (By similarity).
-I- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00633; HHH; 1.
SMART; SM00382; AAA; 1.
SMART; SM00278; HhH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma pneumoniae.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AspRS).
ASPS OR MPN046 OR MP108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D37788; BAA07039.1; -.
EMBL; D17726; BAA04580.1; -.
EMBL; L41342; AAA64873.1; -.
EMBL; AE003772; AAP57005.1;
HSSP; Q06609; 1B22.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspartyl-tRNA
                                                                                                                                                                                                                                                                             "Complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003533; ANA ATPase.
InterPro; IPR000445; HhH.
InterPro; IPR003583; HHH 1.
InterPro; IPR001553; RecA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0011700; Rad51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
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                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Belongs to the reca family. F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-dependent ATPase activity. Underwinds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                   Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                             analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%;
42.1%;
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                                                                                                                                                                                                                                                                                                                        Plagens
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Pred. No. 3.6;
                                                                                                                                                                                                           L-aspartate + tRNA(Asp) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F9E9B21405B15DB0 CRC64;
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                                                                                                                                                                                                                                                                             genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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Usage
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                                                                                                                                                                                                                                                                             bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                      Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by and for commercial
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L outstation -
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are no its content

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RESULT 10
SYD BORBU
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Best Local S
Matches 9
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InterPro; IPR004524; AspS bact.
InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR008994; tRNA-synt 2.
InterPro; IPR002312; tRNA-synt asp.
InterPro; IPR002312; tRNA-synt asp.
InterPro; IPR004365; tRNA-anti.
InterPro; IPR006195; tRNA-ligase_II.
pfam; PF01336; tRNA-synt 2; 2.
pfam; PF01336; tRNA-anti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              051402;
15-DEC-1998
30-MAY-2000
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Lathigra R., White O., Ketchum R.D., Richardson D., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B. Smith H.O., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aminoacyl-tRNA synthetase;
Complete proteome.
SEQUENCE 557 AA; 64114 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1042; TRNASYNTHASP.
TIGREAMS; TIGRO0459; aspS bact; 1.
PROSITE; PS50862; AA TRNA LIGASE II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000013; AAB95756.1; PIR; S73434; S73434.
                                                                                                                                                                                                                                                                                           Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                               burgdorferi."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASPS OR BB0446
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                                                                                                                                                                                              -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                     diphosphate + L-aspartyl-tRNA(Asp)
SUBUNIT: Homodimer (By similarity)
SUBCELLULAR LOCATION: Cytoplasmic.
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d and this statement is not removes requires a license agreement (Sean email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39, Last sequence update)
41, Last annotation updat
thetase (EC 6.1.1.12) (Asp
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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) (Aspartate--tRNA ligase)
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InterPro; HAMAP;

; MF_00044; -; 1 Pro; IPR004524; 1 Pro; IPR004115; (

AspS_bact GAD_dom.

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RESULT 11
SYD_THETN
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Best Local S
Matches 10
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Q8RAI7;
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HAMAP; MF 00044; -; 1.

InterPro; IPR004115; GAD dom.

InterPro; IPR008994; Nucleic acid OB.
                                                                                                                                                                                                                                                                                                                            Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
-I-CATMALTRIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP +
diphosphate + L-aspartyl-tRNA(Asp).
-I-SUBCULTLULAR LOCATION: Cytoplasmic.
-I-SUBCILLULAR LOCATION: Cytoplasmic.
-I-SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
28-FEB-2003 (Rel. 41, Last annotation updat
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Asp
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PIR; |
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InterPro; IPR002312; tRNA-synt asp.
InterPro; IPR004365; tRNA anti.
InterPro; IPR006195; tRNA ligase_II.
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MEDLINE=21992816; PubMed=11997336;
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Bacteria; Firmicutes; Clostridia;
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                                                                      EMBL; AE013085; AAM24458.1; -.
                                                                                                                                                        entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=119072;
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(Aspartate--tRNA ligase)
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Best Local S
Matches 8
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P07252;
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CBP1 OR YJL209W OR J0242 OR HRA654.
CBCharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycee.
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Pfam; PF00152; tRNA-synt_2; 2.
Pfam; PF01336; tRNA anti; 1.
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InterPro; IPR004365; tRNA anti.
InterPro; IPR006195; tRNA_ligase_II.
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InterPro;
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01-NOV-1997
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SEQUENCE 592 AA; 67864 MW; 1621BA9C6BC30381 CRC64;
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PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=84185566; PubMed=6325407; Dieckmann C.L., Homison G., Tzagoloff A.; Rassembly of the mitochondrial membrane s
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed the companies of the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the EM through the E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a yeast nuclear gene (CBP1) involved cytochrome b pre-mRNA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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ol. Cell. Biol. 9:3323-3331(1989).
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an email to license@isb-sib.ch).
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Pred. No. 6.
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Best Local S
Matches
                                                    EMBL; AB010267; AAL81823.1; ALT_INIT.

HAMAP; MF 00210; -; 1.

InterPro; IPR006264; AroA.

InterPro; IPR001986; EPSP synth.

Pfam; PF00275; EPSP synthase; 1.

ProDom; PD001867; EPSP synthase; 1.

TIGRFAMA; TIGR01356; arcA; 1.

PROSITE; PS00104; EPSP_SYNTHASE 1; FALSE_NEG.

PROSITE; PS00185; EPSP_SYNTHASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Germonline; 141821; -.

SGD; S0003745; CBP1.

GO; GO:0005739; C:mitochondrion; IDA.

GO; GO:0003729; F:mRNA binding; IGI.

GO; GO:0009060; P:aerobic respiration;

GO; GO:0006402; P:mRNA catabolism; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z34098; CAA84002.1;
EMBL; Z49484; CAA89506.1;
EMBL; M28067; AAA34456.1;
PIR; S05829; BVBYP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

Wheiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

"The complete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

-I- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.

-I- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT 2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable 3-phosphoshikimate 1-carboxyvinyltransferase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA processing.
SEQUENCE 654 AA;
                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (5-enolpyruvylshikimate-3-phosphate AROA OR PF1699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8U0A0;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AROA PYRFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrococcus furiosus.
  SEQUENCE
                             PROSITE;
Aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sixth step.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 9; Conserv
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     amino acid biosynthesis;
406 AA; 45068 MW; 43P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76171 MW; 2453B03280E1C44D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.48;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
     is; Transferase; Complet
43AACD7FEF97C272 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermococcales; Thermococcaceae;
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                                     Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
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Query Match Best Local

J Man Simus Local Simus 10;

Similarity

39.1%; milarity 47.6%; Conservative

Score 43; DB Pred. No. 20; 3; Mismatches

DB 20;

Length 406; Indels

2;

Gaps

u --

Matches

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PNYVFIRAHDSEVQTRIAKII

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RESULT 14
ARGD_BIFLO
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YMDE_LACLA
  A I
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Best Local (
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

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Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14422-14427(2002).

Proc. Natl. Acad. U.S.A. 99:14427(2002).

Proc. 
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MEDLINE=22294977;

PubMed=12381787;

Schell M.A., Karmirantzou M., Snel B., Vilanova D., B

Schell M.A., Karmirantzou M., Snel B., Vilanova D., B

Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley

Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP, MF_01107; -; 1.
InterPro; IPR005514; Aminotrans_3.
InterPro; IPR005514; Aminotrans_3.
InterPro; IPR00536; ArgD.
Pfam; PF00202; aminotran_3; 1.
TIGRENMS; TIGR00707; argD; 1.
PROSITE; PS00600; AA TRANSFER CLASS_3; 1.
Arginine biosynthesis; Transferase; Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobact
Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium longum.
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28-FEB-2003
YMDE LACLA
Q9CG88; 034131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE014729; AAN24869.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence of Bifidobacterium longum reflects its adaptation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetylornithine aminotransferase (EC
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                                                                                                                                                                                                                                                                                                                                                                       eyridoxal phosphate; co
                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aminotransferases.
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                                                                                                                                                                                                  VPNYVFIRA-----HDSEVQTRIAK 20
                                                                                                                                                   VPNIEFVRAGDKVALHDAFAQTGLGR 206
                                                                                                                                                                                                                                                                                                                                                284
431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                     45615 MW;
                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
84 PYRIDOXAL PHOSPHATE
45615 MW; 1A9245B103521BCE C
                                                                                                                                                                                                                                                                        39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinobacteridae; Bifidobacteriales;
                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                   Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                            Score 43;
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P71566;
01-NOV-1997
01-NOV-1997
10-OCT-2003
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28-FEB-2003
10-OCT-2003
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- SIMILARITY: Belongs to the UPF0176 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=NCDO 2118;
                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Hypothetical protein Rv0943c/MT0969/Mb0968c.
RV0943C OR MT0969 OR MTCY10D7.31 OR MB0968C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U92974; AAB81912.1; -.
EMBL; AE006353; AAK05315.1; -.
PIR; A86777; A86777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Buropean Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delorme C., Goupil-Feuillerat N., Renault P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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Hypothetical protein; Complete proteome.

DOMAIN 125 219 RHODANESE.

CONFLICT 204 204 H -> L (IN)
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                                         Bacteria; Actinobacteria; Actinobacteridae; Actino Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00581; Rhodanese; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00469; -; 1.
InterPro; IPR001763; Rhodanese-like.
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SPECIES=M.tuberculosis;
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             SEQUENCE FROM N.A.
                                      NCBI_TaxID=1773,
                                                                                   Mycobacterium bovis.
                                                                                               Mycobacterium tuberculosis,
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(UPF0176 protein ymdE.
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36849 MW; F987D509415F169A
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47.6%; Pred. No. 1
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  STRAIN=H37Rv;
                                                                       Actinobacteridae; Actinomycetales;
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OCCUPATION ACCUPATION 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98295987;
Cole S.T., Brosch
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BX248337; CAD93829.1;
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37205 MW; F51A5815B5A36136 CRC64;
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GREA MYCPN

ID GREA M

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DE Transe

DE GREA CREA

GREA CREA

COS MYCDI

RP SEQUEN

RC STRAIN
                                                                                                                                                                                                                                    RESULT 18
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                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                        GREA MYCPN
P78019;
01-NOV-1997
01-NOV-1997
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fu
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M.
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi
                                                                                                                                                                                                                                                                                                                                                                                                                                           SITE
ACT SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aoki K.-I., Masuda S.,
Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed property institutions as long as its content use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50173; UMUC; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP; MF_01113; -; 1
InterPro; IPR001126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP000983; BAB65569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE=21456156; PubMed=11572479;
                                                              Mycoplasma pneumoniae 
Bacteria; Firmicutes;
                                                                                            GREA OR MPN401 OR MP437.
                                                                                                                       Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding; Mutator protein;
 STRAIN=ATCC 29342
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPACTOR: Binds 2 magnesium ions per subunit (By similarity) SIMILARITY: Belongs to the DNA polymerase type-Y family. SIMILARITY: Contains 1 umuC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in untargeted mutagenesis. Copies undamaged DNA at stalled replication forks, which arise in vivo from mismatched or mismaligned primer ends. These mismaligned primers can be extended by pollV. Exhibits no 3.5' exonuclease (proofreading) activity. May be involved in translesional synthesis (By similarity). CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Poorly processive, in untargeted mutagenesis. Co
                                                                                                                                                                                                                                                                                                                                               il Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00817; IMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {DNA} (N)
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                                                                                                                                                                                                                                                                                       PNAIFVPMHKEVYTEVSNRIMSII
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353
                                                                                                                                                                                                                                                                                                                                                                                                                                            108
9
                                                                                                                         (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
on elongation factor grea (Trans
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               40125 MW;
                                                                                                                                                                                                                                                                                                                                                                 37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMUC_like.
                                                                 Mollicutes;
                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                   Score 41.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                               MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBSTRATE DISCRIMINATION BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Magnesium; Complete proteome
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                                                                                                                                                                                                                                                                                       94
                                                                 Mycoplasmataceae;
                                                                                                                              n update)
(Transcript
                                                                                                                                                                                                           160
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                                                                                                                                                                                                                                                                                                                                                                      30;
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Kushida N., Oguchi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase
                                                                                                                                                                                                                                                                                                                                                                                   Length 353;
                                                                                                                                cleavage
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                     Мусорlавта
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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Best Local S
Matches 8
                                                                                                                                                                                                                                                          01-FEB-1996
01-FEB-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00829; GREAB 1; 1.

PROSITE; PS00829; GREAB 2; 1.

PROSITE; PS00830; GREAB 2; 1.

Transcription regulation; DNA-binding; Coiled coil; Complete COILED COIL (POTENTIAL).

DOMAIN 8 28 COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

18101 MW; 32448C91712A19C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00105; -; 1.
InterPro; IPR006355; GreA.
InterPro; IPR001437; GreA. GreB.
InterPro; IPR001437; GreA. GreB.
Pfam; PF01272; GreA. GreB. 1.
Pfam; PF03449; GreA. GreB. N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000043; AAB96085.1; PIR; S73763; S73763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herrmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himmelreich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97105885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P21346; 1GRJ.
 Fraser C.M., Godayne J.D., White O., Adams M.D., Clayton R.A., Fraser C.M., Godayne J.D., Weiter O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlayage A.R., Sutton G., Kelley Tritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrich Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEam; PF03449; GreA_GreB_N; 1.
ProDom; PD004918; GreA_GreB; 1.
TIGRPAMs; TIGR01462; greA; 1.
                                                                                                                                                                               Mycoplasma genitalium 
Bacteria; Firmicutes;
                                                                                                                                                                                                                                              Transcription
                                                                                                                                                                                                                                                                                                                            GREA MYCGE
                                                                                                                                                                                                            GREA OR MG282
Peterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Necessary for efficient RNA polymerase transcription elongation past template-encoded arresting sites. The arresting sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as greA or greB allows the resumption of elongation from the new 3'terminus. GreA releases sequences of 2 to 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the greA/greB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotides (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                              49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
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R
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                                                                                                                                                                                                                                           (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation updat)
yn elongation factor grea (Trans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.3%;
                                                                                                                                                                                Mollicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                             tation update)
greA (Transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome
                                                                                                                                                                                Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                   161
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16;
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                                                                                                                                                                                                                                                  cleavage
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                                                          n R.A.,
Kelley J.M.,
                                  Merrick J.M.
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RESULT
KAD4_M
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Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).

-i-FUNCTION: Necessary for efficient RNA polymerase transcription
-i-FUNCTION: Dast template-encoded arresting sites. The arresting
sites in DNA have the property of trapping a certain fraction of
elongating RNA polymerases that pass through, resulting in locked
ternary complexes. Cleavage of the nascent transcript by cleavage
factors such as grea or greB allows the resumption of elongation
from the new 3'terminus. Grea releases sequences of 2 to 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL OUTSTATION the EUROpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01272; GreA GreB; 1.
Pfam; PF03449; GreA GreB N; 1.
ProDom; PD004918; GreA GreB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U39708; AAC71504.1; -. PIR; B64231; B64231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; DNA-binding; Coiled coil; Complete DOMAIN 9 28 COILED COIL (POTENTIAL).

DOMAIN 47 76 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P21346; 1GRJ.
TIGR; MG282; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last
28-FEB-2003 (Rel. 41, Last
Adenylate kinase isoenzyme
                                                                                                                                                                                                                                                                                                KAD4 MOUSE
Q9WUR9; Q9R1X7;
30-MAY-2000 (Re
                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00829; GREAB_1; 1.
PROSITE; PS00830; GREAB_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006359; GreA.
InterPro; IPR001437; GreA GreB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00105; -; 1.
                                                                                                                                                              Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                           transphosphorylase).
AK4 OR AK-4 OR AK3B.
                                                      cloning of
Brain Res.
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                            Mus musculus (Mouse)
             Noma T.
                         SEQUENCE FROM N.A.
                                                                                                            MEDLINE=99033072; PubMed=9813319;
                                                                                 oneda T., Sato M., Maeda M., Takagi H.;
Identification of a novel adenylate kinase system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the greA/greB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced teen the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               NYVFIRAHDSEVQTRIAKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR01462; greA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 AA;
  (B661-AON)
                                                      the fourth adenylate Mol. Brain Res. 62:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                   (Rel.
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
                                                                                                                                                                                                                                                                   39, Creat
39, Last
41, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18162 MW;
                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.3%;
42.1%;
  ç
                                                                                                                                                                                                                                                                                                Created)
    the
                                                                                                                                                                                                                                                      sequence update)
annotation update)
4, mitochondrial (
                                                         γlate kinase.";
62:187-195(1998)
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••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41;
Pred. No.
  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                   Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67E2850CB59BCC5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                  Vertebrata; Euteleostomi;
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                                                                                                                                                                                      Muridae; Murinae; Mus
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Best Local 9
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MGD; MG1:87960; Ak4.
InterPro; IPR006259; Adenylate kin.
InterPro; IPR006850; Adenylate kin.
InterPro; IPR007862; ADK lid.
Pfam; PP00166; ADK; 1.
Pfam; PP05191; ADK lid; 1.
PFRINTS; PR00094; ADENYLTKNASE.
ProDom; PD000657; Adenylate kin; 1.
TIGRFAMB; TIGR01351; adk; 1.
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CONFLICT
CONFLICT
SEQUENCE
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Q9WUS0;
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Transferase; Kinase; GTP-binding; Mitochondrion.

NP BIND
12 20 GTP (BY SIMILARITY).

CONFLICT 68 68 V -> A (IN REF. 2).

CONFLICT 187 187 S -> N (IN REF. 2).

CONFLICT 190 190 V -> M (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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EMBL; AB020239
                                      entities
                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Creat
30-MAY-2000 (Rel. 39, Last
30-MAY-2000 (Rel. 39, Last
Adenylate kinase isoenzyme
                                                                                                                                                                                     STRAIN=Wistar; TISSUE=Forebrain;
MEDLINE=99033072; PubMed=9813319;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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      DEVELOPMENTAL STAGE: EXPRESSED
                         HIPPOCAMPUS
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P08760; 2AK3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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N: Mitochondrial matrix (Potential)
                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
annotation update)
4, mitochondrial (
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Sciurognathi; Muridae; Murinae; Rattus.
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        IN THE CENTRAL NERVOUS SYSTEM
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between
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last amotation update)
Hypothetical protein SPy0538/SpyM3_0382/SPs1471/spyM18_0604.
SPY0538 OR SPYM3_0382 OR SPS1471 OR SPYM18_0604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D87809; BAA77761.1; --
HSSP; D87501; 2AX3.
InterPro; IPR006259; Adenyl kin sub.
InterPro; IPR000850; Adenylate_Kin.
InterPro; IPR007862; ADK_lid.
Pfam; PF005191; ADK_lid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes (serotype M3), and
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Y538_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00094; ADENYLTKNASE.
PRODOM; PD000657; Adenylate kin; 1.
TIGREAMS; TIGR01351; adk; 1.
PROSITE; PS00113; ADENYLATE KINASE;
                                                                                                                                                                                                                                                                             Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Qian Y., Jia H.G., Najar F.Z., Ren C., Zhu H., Song L., Whi Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1314, 198466, 186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes,
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NP_BIND 12 20 GTP (BY SIMILARITY)
                                                                  MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei E
Mammarella N.D., Liu M.-Y., Smoot J.C., Por
Campbell D.S., Smith T.M., McCormick J.K.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
    emergence.";
Proc. Natl.
                                                 phage-encoded toxins,
                                                                                                                                                                                                                STRAIN=MGAS315 / Serotype M3;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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23;
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Porcella S.F., Parkins
K., Leung D.Y.M.,
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                                                   of group A phenotype,
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MEDLINE-21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype group A Streptococcus strains associated with acute rheumatic feathers."
                                                                                                                                                                                                                                                                                                                          SYD BUCAP
P81432;
15-DEC-1998
15-DEC-1998
28-FEB-2003
SEQUENCE FROM N.A.
Thao M.L., Baumann P.;
"Nucleotide sequence c
(Aphid endosymbiont) c
rpsA-himD-tpiA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [3]
SEQUENCE FROM N.A.
STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345;
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InterPro; IPR002795; MAT.
Pfam; PF01941; AdoMet Synthase;
ProDom; PD011777; MAT 1.
Hypothetical protein; Complete I
SEQUENCE 399 AA; 45771 MW; 1
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                                                                                                                                                                          Buchnera aphidicola (subsp. Schizaphis graminum)
Bacteria; Proteobacteria; Gammaproteobacteria; E
Enterobacteriaceae; Buchnera.
                                                                                                                                             NCBI_TaxID=98794;
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SIMILARITY: Belongs to the Adomet synthetase 2 family.
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AE014144; AAM78989.1; -.
AP005145; BAC64566.1; -.
AE009996; AAL97295.1; -.
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COG6 DROME
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EMBL; AE014107; AAM67860.1; -.

HSSP; P21889; 1EQR.

HAMAP; MF 00044; -; 1.

InterPro; IPR004524; AspS_bact.

InterPro; IPR004524; AspS_bact.

InterPro; IPR004115; GAD_dom.

InterPro; IPR004315; Wucleic_acid_OB.

InterPro; IPR004364; tRNA-synt_2.

InterPro; IPR004364; tRNA-synt_asp.

InterPro; IPR004365; tRNA-anti.

InterPro; IPR004365; tRNA_ligase_II.

Pfam: PR02318; CAD: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                           COG6_DROME; STANDARD, Q9V564; Q95RW7; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42) (Ast annotation update)
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Wernegreen J.J., Sandstroem J.P., Mc
"50 million years of genomic stasis
Science 296:2376-2379(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22084549; PubMed=12089438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic (by similaricy).
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - i - CATALYTIC ACTIVITY: ATP + L-aspartate +
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PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacy1-tRNA synthetase; ProteIn biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02938; GAD; 1.
Pfam; PF00152; tRNA-synt_2; 2.
Pfam; PF01336; tRNA_ant1; 1.
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SEQUENCE FROM N.A.
STRALN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.B., Holt R.A., E.
Amanatides P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Moran N.A., Andersson S.G.E.;
is in endosymbiotic bacteria.";
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Hoskins R.A.,
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RA GOOTGE K.A., Lewis S.E., MICHAELE S., ANDLINE, M., PERMELEN, R. SULTON G.G., WOTTHMAN J.R., Yandell M.D., Zhang Q., Chen L.X., RA By Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA BERNANDON, C.R., Miklos G.L.G., RA MARCHAELE, Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA BARTIJ J.P., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Bhiler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Durbin K.J., By Yangeliste C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Hwaland T.J., Hernandez J.R., Houck J., Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alaili M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alaili M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D., RA Mount S.M., Petoro C., Stapleton M., Skupski M.P., Pacleb J.M., RA Markulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A., RA Mount S.M., Petoro C., Stapleton M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Sylreks R., Tector C., Turner R., Venter B., Mang A.H., Wang X., Martei J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Phong S.M., Weinstock G.M., Weinstoach J., Weinstock G.M., Weinstoach J., Wang S.M., Woodage T., Schong W., Zhou S., Zhan M., Zhang G., Zhao Q., Zheng L., Phong S., Zhou D., Scheeler F., Spich H.O., Scheeler J.C., Scheeler J.C., Shao Q., Zheng L., Schen B., Roger M., Zhong G., Zhong S., Zhou X., S
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Sutton G.G.,
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"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley; TISSUB=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P.,
George R.A., Guarin H., Kronmiller B., Pac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, AND ALTERNATIVE SPLICING.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J.,
                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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                                                                                                                    +
                                                                                                                                                                                                                                                                                is composed of eight different subunits and is required golgi morphology and localization (By similarity). SUBCELDILAR LOCATION: Golgi (By similarity). ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2:
                                                                                                            ISOId=Q9V564-2;
SIMILARITY: Belong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Required for normal Golgi function (By similarity) SUBUNIT: Component of the conserved oligomeric Golgi complex
                                        SWISS-PROT entry is
                                                                                                                                                                                                                            IsoId=Q9V564-1;
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                                                                                                                Belongs
                                                                                                            Sequence=VSP_001133, \gs to the COG6 family.
                                                                                                                                                                                                                                Sequence=Displayed;
                                            copyright.
ght. It is produced through Bioinformatics and the EM
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                                                                                                                                                        VSP_001134;
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b J.M., Park S.,
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01-NOV-1997
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EMBL; AB003834; AAM68826.1; -.
EMBL; AY003834; AAM68826.1; -.
EMBL; AY001082; AAL28630.1; -.
FlyBase; FBgn0033401; CG1968.
Hypothetical protein; Transport; Protein transport; Golgi stack;
Membrane; Alternative splicing.
VARSPLIC 315 333 DISDQLQNALGYIADGVCH -> GKIRKCIHYGTK
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J. Bacteriol. 179:2363-2372(1997).
- IPUNCTION: Required for synthesis of the major beta-glucans of the cell wall (By similarity).
- ISUBCELLULAR LOCATION: Type II membrane protein.
- I- SIMILARITY: STRONG, TO KRE6.
                                                                                                                                                                                                                                                     use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no rest
                                                                                                                                              InterPro; IPR008985;
InterPro; IPR005629;
Pfam; PF03935; SKN1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97234650;
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DOMAIN 1 281
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation updat
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Pred. No.
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POLY-PRO.
                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE (POTENTIAL).
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/FTId=VSP_001133.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-DCT-2001 (Includes: Helicase, Methyltransferase].
1A protein [Includes: Helicase, Methyltransferase].
Brome mosaic virus (BMV).
Viruses, BERNA positive-strand viruses, no DNA stage; Bromoviridae;
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"Nucleotide sequence of the brome mosaic virus genome and its
implications for viral replication.";
J. MOL. Biol. 172:369-383(1984).
-i. FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN.
METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
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                                                                                                                                                                                                        InterPro; IPR002588; V methyltransf.
InterPro; IPR000606; Viral helicase1.
Pfam; PF01443; Viral helicase1; 1.
Pfam; PF01660; Vmethyltransf; 1.
                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
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NP_BIND 685 692 ATP (POTENTIAL).
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gontles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G., RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones M., Leather S., McDonald S., McLean J., RA Jones K., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA RA Wolfer K., Rather S., Squares R., Squares S., Stevens K., Sarph S., Stevens K., Squares R., Squares S., Stevens K., Stelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Walsh S.V., Warren T., Whitehead S., RA Wolfens I., Volckaert G., Aert R., Robben J., Grymonprez B., Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., RA Welfjens I., Cadieu E., Dreano S., Hunt C., Moest D., Hilbert H., Ra Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.M., Ra Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Ra Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Ra Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.M., Ra Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.M., Ra Goffeau A., Gaillardin C., Tallada V.A., Garzon A., Thode G., Ra Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Ra C., Cruzado I., Jimenez J., Sanchez M., del Rey F., Benito J., Ra Cert M., Gallardin C., Moore K., Hurst S., Ra C., Cruzado I., Jimenez J., Sanchez M., For
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01-NOY-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Hypochetical protein C22F3.04 in chromosome
                                                                                                                                                                             Hypothetical
TRANSMEM 10
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TRANSMEM 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                           EMBL; Z54285; CAA91069.1; -. PIR; T38187; S62419.
                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                     GeneDB
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                               Pfam; PF00501; AMP-binding;
                                                                                                                                                                                                                                                                                      InterPro; IPR000873; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !- SIMILARITY: TO S. POMBE SPAC56F8.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                          T38187; S62419.
)B_SPombe; SPAC22F3.04;
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                                                                             Similarity 7; Conserv
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1028 1048 סרידים
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POTENTIAL.
YW; A88D03AE0A9E9B99 CRC64;
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16-0CT-2001
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POWPV
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50088; ANK REPEAT; 1.
PROSITE; PS50297; ANK REP_REGION; 1.
Hypothetical protein; Repeat; ANK re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Putative ankyrin-repeat protein FPV224.
                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenain (EC 3.4.22.39) (Endoprotease) (Late L3 23 kDa protein).
Ayian adenovirus type 8 (strain ATCC A-2A) (Fowl adenovirus 8).
                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002110; A) Pfam; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF198100; AAF44568.1;
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                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus
                                                                                                                                                                  16-OCT-2001 (Rel. 40, 0
16-OCT-2001 (Rel. 40, 1
16-OCT-2001 (Rel. 40, 1
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Adenain (EC 3.4.22.39)
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                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=66295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               so C.L., Tulman E.R., Lu Z., genome of fowlpox virus."; irol. 74:3815-3831(2000).
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an email to license@isb-sib.ch).
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Pred. No.
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Pfam; PF00770; Peptidase C5; 1.

PRINTS; PR00703; ADVENOPTASE.

ProDom; PD003705; Peptidase C5; 1.

Pydrolase; Thiol protease; Late protein.

Hydrolase; Thiol protease; Late protein.

ACT_SITE 55 55

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                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2004
15-MAR-2004
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-!- SIMILARITY: Belongs to peptidase family C5
                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22354719; PubMed=12466555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=HF-2;
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                               HAMAP; MF_00044;
InterPro: IPR004
                                                                   EMBL; AP004171; BAC44079.1; -.
                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-II aminoacyl-trnA synthetase family.
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  Q88ay6 pseudomonas Q85c9 campylobact Q7v1y5 rhodopirell Q81th1 staphylococ Q99s87 staphylococ Q9c28 neurospora Q54358 streptomyce Q9m7x2 arabidopsis Q87ze6 pseudomonas Q8dv26 nitrosomona Q8duz7 streptococc Q7v142 prochloroco Q9747 cyprinus ca Q872n5 neurospora Q65173 african swi
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InterPro; IPR002479; CW binding.
InterPro; IPR003218; Glycohydro_70.
Pfam; PP01473; CW binding_1; 9.
Pfam; PP01473; CW binding_1; 9.
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01-NOV-1999
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GTF-S.
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Q84CN4;
Q1.JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1.JUN-2003 (TrEMBLrel. 25, Last annotation update)
Q1.CCT-2003 (TrEMBLrel. 25, Last annotation update)
                           STRAIN=NRRL B-1501;
Kim C.H., Moon J.O., Jang E.K.;
"Gene encoding a dextransucrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus criceti. Plasmid pAM1.
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                                                                                                                                                                  Leuconostoc mesenteroides.
Bacteria; Firmicutes; Lact
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                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=1245;
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       B-1501.";
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                                                                                                                                                                         Lactobacillales;
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Pred. No. 6.3e-10;
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                                  Leuconostoc
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Q88rr4 pseudomonas
Q88rs4 corynebacte
Q89vc8 bradyrhizob
Q99g00 xylella fas
Q14520 homo sapien
Q91uq5 arabidopsis
Q45430 caenorhabdi
Q93wp2 chlamydomon
Q81435 chlamydomon
                                  mesenteroides
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Q91466;
Q91466;
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Q91466;
Q91466
CTEMBLE 1. 15, C)
Q1-QCT-2000 (TEMBLE 1. 15, L)
Q1-QUN-2003 (TEMBLE 1. 24, L)
COLUMN 2003 (TEMBLE 1. 24, L)
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GO; GO:0016757; F:transferase activity, tr
GO; GO:0009250; P:glucan biosynthesis; IEA
InterPro; IPR002479; CM binding:
InterPro; IPR00318; Glyco hydro 70.
Pfam; PF01473; CM binding I; I1.
Pfam; PF01473; CM binding I; 11.
Pfam; PF02324; Glyco hydro 70; 1.
Glycosyltransferase; Transferase.
Glycosyltransferase; Transferase.
                                                                                                                                                                       Q9EZH5;
Q9EZH5;
Q1-MAR-2001
01-MAR-2001
01-JUN-2003
                                     Leuconostoc mesenteroides.
Bacteria; Firmicutes; Lact
NCBI_TaxID=1245;
[1]
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Bacteria; Firmicutes;
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            SEQUENCE FROM N.A.
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                                                                                                                                                        Dextransucrase
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GO; GO:0009250; F:glucan biosynthesis; IEA.
InterPro; IPR002479; CM_binding.
InterPro; IPR003316; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 13.
Pfam; PF01234; Glyco_hydro_70; 1.
Glycosyltransferase; Transferase.
SEQUENCE 1508 AA; 168511 MM; E70CECB57A70
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O52224,

01-JUN-1998 (TrEMBLrel. 06, Created)

01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Q8G9Q2;
Q1-MAR-2003
Q1-MAR-2003
Q1-JUN-2003
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"Leuconostoc mensenteroides B-742CB, a dextransucrase gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR294469; AAG38021.1; -.
GO; GO:0009250; P:glucan biosynthesis; IEA.
InterPro; IPR002479; CM_binding.
InterPro; IPR003316; Glyco.hydro_70.
Pfam; PF01473; CM_binding_1; 13.
Pfam; PF01473; CM_binding_1; 13.
Pfam; PF012324; Glyco.hydro_70; 1.
SEQUENCE 1508 AA; 168542 MW; E2FCFA0F87AE4F3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monchois V., Remaud-Simeon M., Monsan P., Willemot R.M.; "Cloning and sequencing of a gene coding for an extracellular dextransucrase (DSRB) from Leuconostoc mesenteroides NRRL B-1: synthesizing only a a(1-6) glucan."; PEMS Microbiol. Lett. 0:0-0(1998).
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Bacteria; Firmicutes;
                     Leuconostoc mesenteroides.
Bacteria, Firmicutes, Lactobacillales, Leuconostoc
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                                                                                                     Dextransucrase
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Kim H.-S., Kim D.,
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(TIEMMBIrel. 23, Last sequence update)
(TIEMMBIrel. 24, Last annotation update)
use (EC 2.4.1.5) (Fragment).
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Pred. No. 2.2e-06;
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A Bhatnagar R., Singh D.K.S.;
The Consider R., Singh D.K.S.;

R Cloning and Molecular Characterization of Dextransucrase Gen Teleuconostoc mesenteroides NRRL B-512F.";

Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

R EMBL; U81374; AAD10952.1;
R EMBL; U80376; Piglucan biosynthesis; IEA.

R InterPro; IPR002479; CW binding.

R InterPro; IPR003318; Glyco_hydro_70.

Pfam; PF01473; CW binding 1; 12.

Pfam; PF01473; CM binding 1; 12.

Pfam; PF02324; Glyco_hydro_70; 1.

Pfam; PF02324; Glyco_hydro_70; 1.

Pfam; PF02324; Glyco_hydro_70; 1.
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                                        Q8KRE1;
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"Molecular characterisation of DSR-E, synthesising dextransucrase with two J. Bacteriol 184:5753-5761(2002).
                01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Dextransucrase DsrD (EC
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Bacteria; Firmicutes; Lact
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; AX017384; AAG61158.1;
REGO; GO:0016757; F:transferase activity, transferring glycos;
R GO; GO:0009250; P:glucan biosynthesis; IEA.
R GO; FO:0009250; P:glucan biosynthesis; IEA.
R Fo:0009250; P:glucan biosynthesis; IEA.
R Fo:0009250; P:glucan biosynthesis; IEA.
R Fo:0009250; P:glucan biosynthesis; IEA.
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InterPro; IPR002479; CW binding-InterPro; IPR003318; Glyco-Mydro-70. Pfam; PF01473; CW binding-1; 11. Pfam; PF01324; Glyco-Mydro-70; 1.
      Q9LCJ7
Q9LCJ7;
Q9LCJ7;
01-OCT-2000
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Q9WXJ5;
01-NOV-1999
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SEQUENCE
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Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
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Plasmid pAM1.
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HSSP; P06278; IVJS.

GO; GO:0009250; P:glucan biosynthesis; IF

R InterPro; IPR002479; CW_binding.

R InterPro; IPR003318; Glyco_hydro_70.

R Pfam; PF02324; Glyco_hydro_70; 1.

PFONTRNCE 1016 AA; 110344 MW; 8896EFD
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MEDLINE=20169623; PubMed=10705445;
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009250; F:transferase activity; IEA.
GO; GO:0009250; F:glucan biosynthesis; IEA.
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02224; Glyco_hydro_70; 1.
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Hanada N., Fukushima K., Nomura Y., Senpuku H., Hayakawa M.,
Mukasa H., Shiroza T., Abiko Y.;
Mukasa H., Shiroza T., Abiko Y.;
"Cloning and nucleotide sequence analysis of the Streptococcus
sobrinus gtfU gene that produces a highly branched water-solub
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WEDLINB=20231779; PubMed=10768934;

MEDLINB=20231779; PubMed=10768934;

Fujiwara T., Hoshino T., Ooshima T., Sobue S., Hamada S.;

"Purification, characterization, and molecular analysis of the
"Purification, characterization, and molecular analysis of the
                                                                                                                                                                                               encoding glucosyltransferase from Streptococcus Infect. Immun. 68:2475-2483 (2000).

EMBL; AB025228; BAA95201.1; -
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:glucan biosynthesis; IEA.
InterPro; IER002479; CW binding.
InterPro; IER002479; CW binding.
InterPro; IER003318; Glyco hydro_70.
Pfam; PF01473; CW binding_1; 16.
Pfam; PF01473; CW binding_1; 16.
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Bacteria; Firmicutes;
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InterPro; IPR00318; Glyco hydro_70.
Pfam; PF01473; CW_binding_I; 9.
Pfam; PF02324; Glyco hydro_70; 1.
SEQUENCE 1290 AA; 145590 MW; 359
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PIR; JC5473; JC5473.
GO; GO:0009250; P:glucan biosynthesis;
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MEDLINE=97136686; PubMed=8982063;
Monchois V., Willemot R.M., Remaud-Simeon M., Croux C., Monsan P.;
Monchois v., Willemot R.M., Remaud-Simeon M., Croux C., Monsan P.;
"Cloning and sequencing of a gene coding for a novel dextransucrase from Leuconostoc mesenteroides NRRL B-1299 synthesizing only alpha (6) and alpha (1-3) linkages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LСН3
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Bacteria; Firmicutes; Lactobacillales; Leuconostoc
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01-OCT-2003
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01-NOV-1996
                                                                                                                                         SEQUENCE
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l Similarity
16; Conserv
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Pred. No. 9.4e
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Mismatches
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                                       No. 3
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Best Local
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Q54178; Q54247;
01-NOV-1996 (Tre
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01-NOV-1996 (
01-NOV-1996 (
01-JUN-2003
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EMBL; M89776; AAA26969.1; -.
PIR; B41898; B41898.
                  SEQUENCE FROM N.A.
MEDLINE=95122197; PubMed=7822030;
Simpson C.L., Giffard P.M., Jacqu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96157084; PubMed=8586195;
Vickerman M.M., Sulavik M.C., Clewel
"Molecular analysis of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus gordonii Challis.
Bacteria; Firmicutes; Lactobacillales;
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01-JUN-2003
                                                                                                                                   Streptococcus
                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                               Streptococcus salivarius
                                                                                                                                                                                                                         Glucosyltransferase
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                                                                                                         NCBI_TaxID=1304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phase variants.
    "Streptococcus salivarius ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 174:3577-3586(1992).
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337; PubMed=1534326;
Tardif G., Clewell D.B.;
                                                                                                                                                                                                                         precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.5%;
80.0%;
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                                                                                                                                                            Lactobacillales;
                                                                                                                                                                                                                                       01, Created)
01, Last sequence update)
24, Last annotation update)
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Last annotation update)
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                            Jacques N.A.;
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Pred. No.
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PIR; T30858; T30858.

GO; GO:0016740; F:transferase activity; IE
GO; GO:0016740; F:transferase activity; IE
GO; GO:0016740; F:transferase activity; IE
GO; GO:0016740; F:transferase activity; IE
GO; GO:0009250; P:glucan biosynthesis; IEP
InterPro; IPR004829; Csurface_antigen.
InterPro; IPR003479; CW binding.
InterPro; IPR003318; Glyco hydro_70.
Pfam; PF01473; CW binding.; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
ProDom; PD153432; Csurface_antigen; 1.
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ALPHA AMYLASES AND RABBIT G.
EMBL; Z11872; CAA77898.1; -
EMBL; Z11873; CAA77901.1; -
EMBL; M64111; AAA26897.1; -
PIR; S22737; S22737.
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Q00599;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                               glucosyltransferase genes in Streptococcus salivarius ATCC 25975.";
J. Gen. Microbiol. 137:2577-2593 (1991).
- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
- PUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
- PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
THEIR ABILLITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amoutation update)
Glucosyltransferase S precursor (EC 2.4.1.5) (GTF) (Dextransucrase)
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Signal; Transferase.
SIGNAL 1
                                                                                                                                                                                                                                                         MEDLINE=93381463; PubMed=8371114; Giffard P.M., Allen D.M., Milward C.P., Simpson C.L., Jacques N. Giffard P.M., Allen D.M., Milward C.P., Simpson C.L., Jacques N. "Sequence of the gtf gene of Streptococcus salivarius ATCC 2597 evolution of the gtf genes of oral streptococci."; J. Gen. Microbiol. 139:1511-1522(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92148377; PubMed=1838391;
Giffard P.M., Simpson C.L., Milward C.P., Jacques N.A.;
"Molecular characterization of a cluster of at least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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GO:0016757; F:transferase activity, transferring GO:0009250; P:glucan biosynthesis; IEA. erPro; IPR002479; CW_binding.
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Submitted (FEB-1998) to the EMBL/GenBank/D
EMBL; AF049609; AACO5156.1; -.
PIR; T30552; T30552.
GO; GO:0016740; F:transferase activity; IE
GO; GO:0009250; F:glucan biosynthesis; IEA
InterPro; IFR002479; CW_binding.
InterPro; IFR003318; Glyco hydro_70.
Pfam; PF01473; CW_binding_1; 7.
Pfam; PF01473; CW_binding_1; 7.
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01-AUG-1998 (TrEMBLrel. 07, Last
01-JUN-2003 (TrEMBLrel. 24, Last
Glucosyltransferase N (Fragment).
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Pfam; PP01473; CW_binding_T; 13.

Pfam; PP02324; Glyco hydro_70; 1.

Transferase; GlycosyItransferase; Signal; Repeat; Dental caries.
                                                                                                                                                                                           Q55264; PRELIMINARY;
Q55264; PRELIMINARY;
Q1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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                        SEQUENCE FROM N.A.
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                                                                                                            Bacteria; Firmicutes;
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1599 AA;
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         PubMed=7822030;
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                                                                                                                                                                           precursor.
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                                                                                                            Lactobacillales;
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Pred. No.
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Pred. No. 0.
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GLUCOSYLTRANSFERASE S.
                                                                                                                                                                                                                                                                                       PRT;
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Best Local
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Q00600;
01-NOV-1996 (TIEMBLIEL.
01-NOV-1996 (TIEMBLIEL.
01-JUN-2003 (TIEMBLIEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson C.L., Giffard P.M., Jacques N.A.;
"Streptococcus salivarius ATCC 25975 possesses at least two genes coding for primer-independent glucosyltransferases.";
Infect. Immun. 63:609-621 [1995].
EMBL; L35495; AAC41412:1;
-PIR; T30857; T30857.
   DOMAIN
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                                                                                                                                                                                                                                                    PIR; A44811. A44811.
GO; GO:000550; F:transferase activity, tra
GO; GO:000950; F:glucan biosynthesis; IEA.
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 11.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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SIGNAL 1
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InterPro; IPR003318; Glyco hydro_
Pfam; PF01473; CW binding 1; 7.
Pfam; PF02324; Glyco hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosyltransferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

1- CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL)(N+1).

-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Giffard P.M., Simpson C.L., Milward C.P., Jacques N.A.; "Molecular characterization of a cluster of at least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 25975;
MEDLINE=92148377; PubMed=1838391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus salivarius
                                                                                                                                                                                                                                Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DISEASE: DENTAL CARIES. EMBL; Z11873; CAA77900.1; -. EMBL; M64111; AAA26896.1; -.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
referase I (EC 2.4.1.5) (GTF) (Dextransucrase)
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                                                                                             Glycosyltransferase; Repeat;
307 1482 6 DIRECT REP
307 1336 PEPEAT 1.
339 1352 PEPEAT 2.
372 1403 PEPEAT 3.
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BYBL; D13858; BAA02976.1; -.

G0; G0:0016757; F:transferase activity, transferring glycosyl. ..

G0; G0:0009250; P:glucan biosynthesis; IEA.

InterPro; IPR002479; CM binding.

InterPro; IPR002479; CM binding.

Pfam; PP01473; CM binding 1; 13.

Pfam; PP02324; Glyco_hydro_70; 1.

Glycosyltransferase; Signal; DTTTANSFERASE.

Glycosyltransferase; Signal; DTTTANSFERASE.

BOTTTANSFERASE.
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Q55263;
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Sato S., Inoue M., Handa N., Alzawa Y., I
"DNA sequence of the glucosyltransferase
Streptococcus sobrinus.";
DNA Seq. 4:19-27(1993).
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amino-acid sequences of water-insoluble-glucan synthetase from Streptococcus sobrinus ATCC 33478.";
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GO; GO:0009250; P:glucan biosynthesis; InterPro; IPR002479; CW binding.

InterPro; IPR003318; Glyco hydro_70.

Pfam; PF01473; CW binding_1; 13.

Pfam; PF02324; Glyco hydro_70; 1.

Pfam; PF02324; Glyco hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The gene encoding alternansucrase, a sucrose glucosyltransferase from Leuconostoc mesenteroides NRRL B-1355."; FEMS Microbiol. Lett. 182:81-85 (2000).

EMBL; AJ256173; CAB65910.2; -.
GO; GO:0016757; F:transferase activity, transferring glycosyl. ..; GO; GO:0016757; F:glucan biosynthesis; IEA.

InterPro; IPR002479; CM binding.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01473; CM binding_1; 11.
Pfam; PF02224; Glyco hydro 70; 1.
Glycosyltransferase; Transferase.
SEQUENCE 2057 AA; 228987 MW; 62BCE9385D9A11BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NRRL B-1355;
MEDLINE=20080809; PubMed=10612736;
Arguello-Morales M.A., Remaud-Simeon M.,
Willemot R.M., Monsan P.;
"Sequence analysis of the gene encoding;
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01-MAY-2000
Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01~MAR-2001
01-JUN-2003
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                                                                                                               01-JUN-2003 (TrEMB
10A19I.11 protein.
10A19I.11.
                                                                                                                                                                                     01-NOV-1999
01-NOV-1999
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(TYEMBLIEL 16, Last sequence update)
(TYEMBLIEL 24, Last annotation update)
case (EC 2.4.1.140).
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Pred.
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Pred. No.
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SEQUENCE FROM N.A.
STRAIN=cv. Lemont;
Vysotskaia V.S., Sc
Liu S., Lee J., Tor
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SMART; SM00271; DnaJ; 1.
PROSTIE; PS50076; DNAJ 2; 1.
SEQUENCE 1442 AA; 159434 MW;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001697; AAD35210.1; -.
PIR; C72417; C72417.
TIGR; TM0116; -.
GO; GO:0003590; F:double-stranded DNA binding; IEA.
GO; GO:00016301; F:kinase activity; IEA.
GO; GO:0004556; F:xylulokinase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0006265; P:DNA topological change; IEA.
GO; GO:0005997; P:xylulose metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MSB8 / DSW 3109;

MEDLINE-99207316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

McDonald L., Utterback T.R., Malek J.A., Fhillips C.A., Richardson D.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gramene; Q9XHV5;
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                                                                                                                                                                                                                   InterPro; IPR000577; FGGY kin.
InterPro; IPR001448; SASP.
InterPro; IPR005000; Xylulokinase.
Pfam; PF00370; FGGY; 1.
Pfam; PF00370; FGGY C; 1.
TIGREPAMS; TIGR01312; XylB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugar kinase,
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01-OCT-2003
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                                                                                                                                          PROSITE; PS00933; FGGY_KINASES_1; PROSITE; PS00445; FGGY_KINASES_2; PROSITE; PS00304; SASP_1; 1.
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                                                                                                   SEQUENCE
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Similarity
8; Conserv
                                                                                                   Complete proteome. 492 AA; 54405
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                                                                                                   54405 MW;
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Pred. No.
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Kremenetskaia I., Oji
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Glodek A., Gong F., Gorrell J.H., Glasser K.,
RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li J., Li J.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Palazzolo M., Pittman K.S., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Samders R.D., Scheler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhong W., Zhou X., Zhong Y., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Idegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Paragas V., Park S., Patel S., Pfeiffer B.,
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Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
Amonatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter R.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Decory V., Borger B., Bayraktaroglu D., Beasley E.M.,
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Neoptera; Edopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
SEQUENCE 279 AA; 30459 MW;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003584; F:damaged DNA binding; IEA.
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GO; GO:0006310; F:DNA repair; IEA.
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CG10051 protein.
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                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0034437; CG10051.
GO; GO:0008233; F:ppridase activity;
GO; GO:0006508; F:proteolysis and pept
InterPro; IPR007484; Peptidase_M28.
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01-JUN-2002
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Ephydroidea; Drosophilidae; Drosophila.
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G0:000524; F:ATP binding; IEA.
G0:0003584; F:damaged DNA binding; IEA
G0:0003694; F:DNA dependent ATPase act:
G0:0000166; F:nucleotide binding; IEA.
G0:0006310; P:DNA recombination; IEA.
G0:0006311; P:DNA repair; IEA.
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Pred. No. 63;
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RA Adams M.D. Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.M.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q. Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q. Chen L.X.,
RA Ballew R.M., Base A., Barter E.G., Helt G., Nelson C.R., Miklos G.D.G.,
RA WARN K.H., Doyle C., Barter E.G., Helt G., Nelson C.R., Miklos G.D.G.,
RA Ballew R.M., Base A., Barkendale J., Bayraktaroglu L., Beasley S.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan A., Boulke H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borson K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Posler C., Gabrielian A.R., Gayy N.S., Gelbart W.M., Glasser K.,
RA Durbin K.J., Evangelists C.C., Ferraz C., Ferriera S., Felschmann W.,
RA Posler C., Gabrielian A.R., Gayy N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Houston K.A., Howland T.J., Wein, H., Ibeysam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,
RA Kimmel B.E., Siden K.A., Sixon K., Nussek M.P., Smith T.,
RA Mculut S.M., My M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Kimst S.M., My M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Kimst S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao Q. A.,
RA Mang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao Q. A.,
RA Mang S., Posladas A., Posladas M.P., Shou S., Zheng 
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Q9A9H5 PRELIMINARY;
Q9A9H5; PRELIMINARY;
Q1_JUN-2001 (TrEMBLrel. 17, I
01_JUN-2001 (TrEMBLrel. 24, I
01_JUN-2003 (TrEMBLrel. 24, I
Hypothetical protein CC1005
CC1005 OR SST1.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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DT 01-JU
DB Prote
GN PROA.
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Q9AQR3;
01-JUN-2001
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"Identification of lipopolysaccharide O antigen synthesis genes
required for attachment of the S-layer of Caulobacter crescentus.";
Microbiology 147:1451-1460 (2001).

Microbiology 147:2451-1460 (2001).

MICROBIOS778; BAK22989.1; -.

EMBL; AF062345; BAK72615.1; -.

EIR; A87374; A87374.

TIGR; CC1005; -.
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Elly B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathewa M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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                       "Novel oxidatively stable subtilisin-like serine | alkaliphilic Bacillus ssp.: enzymatic properties, evolutionary relationships."; Biochem. Biophys. Res. Commun. 279:313-319(2000).
                                                                                                                                                            MEDLINE=20568675; PubMed=11118284;
Saeki K., Okuda M., Hatada Y., Kobayashi T.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                  Bacillus sp. 9860.
Racteria; Firmicutes;
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SEQUENCE 498 AA; 51975 MW; 42B55222BD851A67 CRC64;
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STRAIN=ATCC 19089 / CB15, and CB15N / NA1000;
MEDLINE=98292737; PubMed=9620954;
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Caulobacteraceae; Caulobacter.
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US-09-210-361-6; Sequence 6, Application US/09210361; Patent No. 6284479; GENERAL INFORMATION:
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Matches
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SEQ ID NO 4
LENGTH: 545
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Patent No.
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Best Local (
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LENGTH: 1430
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Patent No. 6127602
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Best Local Similarity
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APPLICANT: Nichols, Scott E.
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/008,172
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starch
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0358D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388 CURRENT APPLICATION NUMBER: US/09/604,957 CURRENT FILING DATE: 2000-06-28 PRIOR APPLICATION NUMBER: 00201871.1 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
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NUMBER OF SEQ ID NOS: 2
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18; Conserv
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RAHAOUI, HAKIM
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Pred. No. 3.2e
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RESULT 4
US-09-740-274-6
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CURRENT APPLICATION NUMBER: US/09/740,274

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 09/210,361

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: 09/007,999

PRIOR FILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-6

PRIOR PILING DATE: 1995-06-07

PRIOR PILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 09/09,620

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PRIOR APPLICATION NUMBER: 09/09,620

PRIOR APPLICATION NUMBER: 09/09,620

PRIOR PILING DATE: 1995-06-07

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CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/09,620
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
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SOFTWARE: FastSEQ fo
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EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
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PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/C
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TITLE OF INVENTION: Glucan-containing Compositions and Paper
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EARLIER FILING DATE: 1998-01-16
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Local Similarity 90.0%;
es 18; Conservative
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Pred. No.
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                                                                                                                                                            RESULT 7
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                                                                     Sequence 2, Application US/09210361
Patent No. 6284479
GENERAL INFORMATION:
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LENGTH: 1
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Streptococcus mutans
-09-007-999-2
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TITLE OF INVENTION: Substitutes for Modified Starch and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0356D
CURRENT APPLICATION NUMBER: US/09/007,999
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER APPLICATION NUMBER: 08/478,704
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CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
        APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
FILE REFERENCE: 0357CR
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77.3%;
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Pred. No. 2e-05;
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US-09-740-274-2
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR PRIOR APPLICATION NUMBER: 09/007,704
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
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GENERAL INFORMATION:
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Best Local Similarity 77.3%;
Matches 17; Conservative
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                                                                            Matches
                                                                                                                 Query Match
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PRIOR TILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows
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PRIOR APPLICATION NUMBER: 08//
PRIOR APPLICATION NUMBER: 08//
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EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
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PRIOR FILING DATE: 1998-01-16
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TITLE OF INVENTION: Glucan-containing Compositions and Paper
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TYPE: PRT
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NUMBER OF SEQ ID NOS: 6
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EARLIER FILING DATE: 1995-06-07
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                                                                                              ocal Similarity
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APPLICATION NUMBER: 09/009,620
FILING DATE: 1998-01-20
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VPSYSFIRAHDSEVQDLIADII 573
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Pred. No.
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Pred. No. 2e-05;
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Best Local S
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                                                                     EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
                                                                                                                                                                           FILE REFERENCE: 0357CR
CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
                  EARLIER
EARLIER
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TITLE OF INVENTION: Substitutes for Modified Starches
TITLE OF INVENTION: Latexes in Paper Manufacture
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TELEX: 26547
INFORMATION FOR SEQ ID NO: 2:
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,824
FILING DATE:
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APPLICANT: Giffard, Philip Morrison
APPLICANT: Jacques, Nicholas Anthony
TITLE OF INVENTION: Increase Stored Carbohydrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: AU PM7643
FILING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
TELEPAX: 61 2 957 6288
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LENGTH: 1577 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Griffith Hack & Co
STREET: Level 8, 168 Walker Street
CITY: No. 5981888th Sydney
STATE: New South Wales
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                                                                                                                                                                                                                                                                                                                                                                                                                                        661 NYIFVRAHDSEVQAVLANII 680
                                                      FILING DATE: 1998-01-20
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                                   APPLICATION NUMBER: 08/485,243
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70.0%;
09/008,172
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Pred. No.
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US-09-740-274-4
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CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR PILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                     GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
                                                                                                                       Sequence 6, Application US/09604957 Patent No. 6486314
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EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
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PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 08/4
PRIOR PILING DATE: 1995-06-07
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TITLE OF INVENTION: Glucan-containing Compositions and Paper
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SOFTWARE: FastSEQ for Windows Version
                                APPLICANT: DIJKHUIZEN, LUBBI
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
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TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL FILE REFERENCE: BO 43388
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                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: streptococcus mutans
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                                                                       LUBBERT
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Pred. No. 9.
                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                           DB 4;
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                                                                                                                                                                                                                                                                                                                                         Length 1375;
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                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                           0;
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CURRENT APPLICATION NUMBER: US/09/604,957

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-604-957-7
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                                                                                                                                                                                                                                                                                                                                                               US-09-604-957-3
                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0
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SEQ ID NO 6
LENGTH: 584
                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09604957 Patent No. 6486314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Leuconostoc mesenteroides 09-604-957-6
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                                                         SEQ ID NO 3
                                                                                                        TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR ETLING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 00201871.1 PRIOR FILING DATE: 2000-05-25 NUMBER OF SEQ ID NOS: 17
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PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VAN GEEL-SCHUTTEN,
APPLICANT: DIJKHUIZEN, LUBBEI
APPLICANT: RAHAOUI, HAKIM
                                                                           SOFTWARE:
                                                                                            NUMBER OF SEQ ID NOS: 17
LENGTH: 1278
TYPE: PRT
ORGANISM: Lactobacillus reuteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 IPNYSFVRAHDYDAODPISK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                        144 IPNYSEVRAHDNNSQDQIQNAI 165
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                                                                         PatentIn Ver. 2.1
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55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; I
Pred. No. 0.
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Pred. No. 0.0032;
4; Mismatches
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APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: NOMURA, MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR PILLING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
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Query Match
Best Local Similarity
Thes 6; Conserve
                                                                            ; TYPE: PRT; ORGANISM: Bacillus
US-09-509-814A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/499,203
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09499203 Patent No. 6570065
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KOSSMANN, Jens
APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
FILE REFERENCE: 147-196P
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
                                                                                                                                                              SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Leuconostoc mesenteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2057
                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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HITOMI, JUN
            40.9%;
ilarity 28.6%;
Conservative
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55.0%;
             Score 45; DB Pred. No. 13; 9; Mismatches
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Pred. No. 0.032;
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Pred. No. 0.018;
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                                               Length 639;
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US-09-107-532A-5511
                                                                                                RESULT 18
US-09-328-352-5587
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Best Local Similarity
Watches 7; Conserve
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Sequence 5587, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5511, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 5511:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...183
SEQUENCE DESCRIPTION: SEQ ID NO: 5511:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                               40 IFWEAHHSQIYTTLAKL 56
                                                                                                                                                                                                                  5 VFIRAHDSEVQTRIAKI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                         Conservative
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Pred. No. 10;
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AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                              Length 183;
                                                                                                                                                                                                                                                           Indels
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Sequence 2, Application US/09330611

Patent No. 6248874

GENERAL INFORMATION:
APPLICANT: FREY, Perry A.
APPLICANT: FREY, Perry A.
TITLE OF INVENTION: DNA MOLECULES ENCODING BAY
FILE REFERENCE: 032026/0476

CURRENT APPLICATION NUMBER: US/09/330,611
CURRENT FILLING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 09/198,942

EARLIER FILLING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 32
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US-09-579-181-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5587
                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                ; TYPE: PRT ; ORGANISM: Clostridium subterminale US-09-330-611-2
                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
                                                                                                                                                                                                                                                                                                                                                 US-09-330-611-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Pate
; SEQ ID NO 1
; LENGTH: 3118
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SEQ ID NO 5587
LENGTH: 652
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Patent No. 636537
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                                                                                                SEQ ID NO 2
LENGTH: 416
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REPERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
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Pred. No. 44;
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Pred.
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Pred. No. 2
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     DB 3;
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                                                                                          RESULT 23
US-09-489-039A-9606
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APPLICANT: Gary Breton et. al
APPLICANT: GARY BRETON et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FREY, PETY A.
APPLICANT: RUZICKA, Frank J.
APPLICANT: RUZICKA, Frank J.
TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
FILE REFERENCE: 032026/0476
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SEQ ID NO 11050
LENGTH: 545
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                                                    Sequence 9606, Application US/09489039A Patent No. 6610836
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LENGTH: 48
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Patent No. 624887
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/330,611
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 09/198,942
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Clostridium subterminale
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Local Similarity 33.3%;
es 7; Conservation
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Pred. No.
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; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9606
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US-08-911-321-4
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/096
PILING DATE: July 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: IAN C. MCLeod
REGISTRATION NUMBER: 20,93
REFERENCE/DOCKET NUMBER: MAREINERENCE/DOCKET 
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CORRESPONDENCE ADDRESS
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                              ORIGINAL SOURCE:
                                                                                           ANTI-SENSE:
ORGANISM:
STRAIN: 1
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CLASSIFICATION: 435
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CITY: Okemos
                                                                                                                                                                                                                                            TYPE: Amino Acid
STRANDEDNESS: Sir
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                                Feline herpesvirus-1
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Pred. No.
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52;
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RESULT 26
US-08-413-118-4
                                                                                                 8
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NAME: US/08/220,151
PILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2540
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-333
TELEFAX: 425066 CURTMS
INFORMATION FOR SEG ID NO: 4:
CECHTMATION FOR SEG ID NO: 4:
                                                                                                                                                                                                             US-08-220-151-4
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Patent No. 5529780
GENERAL INFORMATION:
                                                                                                                                         Matches
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Best Local :
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Paoletti, Enzo
APPLICANT: Limbach, Keith J.
TITLE OF INVENTION: NUCLEGIIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS GB, gC AND GD AND USES THEREFOR NUMBER OF SEQUENCES: 91
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1041 amino aci
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                                                                                                                                                                                                                            MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
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CITY: New York
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                                                                                                                                                                                                                                                                           STRANDEDNESS:
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STREET: 530 Fifth Avenue
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                                                                     641 YDYIQAHVNEMLSRIA 656
                                                                                           4 YVFIRAHDSEVQTRIA 19
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8; Conserv
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N-terminal
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50.0%;
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Patent No. 6017542
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 840-33
TELEPAX: (212) 840-0712
INFORMATION FOR SEQ ID NO:
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APPLICANT: LIMBACH, KI
TITLE OF INVENTION: NI
TITLE OF INVENTION: CJ
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APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                 APPLICANT: PAOLETTI,
APPLICANT: LIMBACH, I
TITLE OF INVENTION: I
TITLE OF INVENTION: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                             NUMBER OF SEQUENCES: 1
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                                                    COUNTRY: UN
                                                                                        STATE:
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                                                                                                                            STREET:
                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEW YORK
                                                                       NEW YORK
UNITED STATES OF AMERICA
                                                                                                                            E: CURTIS, MORRIS
530 FIFTH AVENUE,
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                                                                                                                                                                                 KEITH J.

NUCLEOTIDE AND AMINO ACID SEQUENCES OF
CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.4%; Score 40; DB 1; Le 50.0%; Pred. No. 1.7e+02; c. Mismatches 3;
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                                                                                                                              & SAFFORD, P.C.
25TH FLOOR
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US-09-071-035-420
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 420,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                             TELEPHONE: (301) 309-8512
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                            REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: A. Andere Brookee
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/473,446
                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
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CITY: Rockville
STATE: Maryland
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SOFTWARE: Patenti
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                ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                 Diskette,
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                                                                                                                                                                                                                                                                                                                                    MSDOS version 6.2
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                                                 420:
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                                                                                                                       PB369P2
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Pred. No. 1.7e+02;
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Best Local Similarity
Matches 9; Conserv
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                                                                       US-09-134-000C-6043
GENERAL INFORMATION:
APPLICANT: LYAND DOUCETTE-Stamm et al
APPLICANT: LYAND DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                        Sequence 6043, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 418, Application US/09071035
Patent No. 6448043
                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO: 418:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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TOPOLOGY: 111
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CLASSIFICATION:
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FITTLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6043
LENGTH: 1278
TYPE: PRT
CORGANISM: Enterococcus faecalis
US-09-134-000C-6043
US-09-134-000C-6043
US-09-134-000C-6043
US-09-134-000C-5043
US-09-134-000C-5043

Query Match
Best Local Similarity 56.2%; Pred. No. 2.2e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Db 1100 VDNFVRIRPNDQEVVT 1115
Search completed: May 4, 2004, 09:14:12
Job time: 15 secs
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Result
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16. 47 42.7 557 12 US-10-222-122A-64099 Sequence 60.099, A 45 40.9 305 12 US-10-46-479-8 Sequence 80.099, A 45 40.9 5305 12 US-10-46-479-8 Sequence 80.099, A 45 40.9 5305 12 US-10-46-479-8 Sequence 80.5, Appli 40.0 539 5727 10 US-10-222-122A-64519 Sequence 31.75, A 59 10 US-10-222-122A-65116 Sequence 13.75, A 14 39.1 39.1 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 39.1 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 39.1 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 39.1 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 39.1 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 39.1 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 39.1 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 37.3 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 37.3 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 37.3 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 37.3 129.1 US-10-222-122A-65213 Sequence 13.75, A 14 37.3 129.1 US-10-222-122A-67747 Sequence 13.75, A 14 37.3 129.1 US-10-222-122A-67747 Sequence 13.75, A 14 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 41 37.3 129.1 US-10-222-122A-67747 Sequence 23.7 Appli 42.7 US-10-222-122A-67747 Sequence 23.7 Appli 42.7 US-10-222-122A-67747 Sequence 23.7 Appli 42.7 US-10-222-122A-67747 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.7 US-10-222-122A-6774 Sequence 23.7 Appli 42.
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APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: B043388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
NUMBER OF SEQ ID NOS: 19
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                PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR PELICATION NUMBER: 09/007,999
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/008,172
PRIOR APPLICATION NUMBER: 09/008,172
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Best Local Similarity
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LENGTH: 545
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CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
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TITLE OF INVENTION: Glucan-containing Compositions and Paper
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      FILING DATE:
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Pred. No. 1.9e
1; Mismatches
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US-10-012-600B-178
US-10-369-493-13077
US-10-425-114-59903
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US-09-815-242-12553
US-09-815-242-12816
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US-10-282-122A-70953
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Sequence 178, App
Sequence 13077, A
Sequence 59903, A
Sequence 184196,
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Sequence 75, Appl
Sequence 1253, A
Sequence 12816, A
Sequence 44049, A
Sequence 7953, A
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Sequence 6826, Ap
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FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION UNMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
SOPTWARE: PATENTIN VET: 2.1
SEQ ID NO 11
LENGTH: 522
TYPE: DET
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions and Paper FILE REFERENCE: 0357CRD
CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT TILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR PILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR APPLICATION NUMBER: 09/478,704
PRIOR PILING DATE: 1998-01-16
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/478,704
PRIOR APPLICATION NUMBER: 09/478,704
PRIOR APPLICATION NUMBER: 09/485,243
PRIOR APPLICATION NUMBER: 09/485,243
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR FILING DATE: 1995-06-07
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US-09-740-274-2
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APPLICANT: VAN GEEL-SCHUTTEN,
APPLICANT: DIJKHUIZEN, LUBBER
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
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Patent No. US20020155568A1
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PRIOR FILING DATE: 1995-C
NUMBER OF SEQ ID NOS: 6
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ORGANISM: Leuconostoc mesenteroides
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Local Similarity 90.0%;
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Pred. No. 5.
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SEQ ID NO 4
LENGTH: 1375
TYPE: PRT
                                                                                                 Sequence 13, Application US/09995749A Patent No. US20020155568A1 GENERAL INFORMATION:
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Best Local :
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PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/
                                                APPLICANT: VAN GEEL-SCHUTTEN, GI
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: BO43388-CIP
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NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
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PRIOR APPLICATION NUMBER: 09/007,999
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PRIOR APPLICATION NUMBER: 09/210,361
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CURRENT FILING DATE: 2000-12-19
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TITLE OF INVENTION: Glucan-containing Compositions and
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Streptococcus mutans
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                                                                                                                                                                                                                                                                                            Local Similarity 72.
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                                                                                    GERRITDINA HENDRIKA
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US-09-995-749A-2
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN,
APPLICANT: DIJKHUIZEN, LUBBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 13
LENGTH: 535
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
                                                         TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES FILE REFERENCE: BO43388-CIP CURRENT APPLICATION NUMBER: US/09/995,749A CURRENT FILING DATE: 2001-11-29
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CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
                                                                                                                                    APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VAN GEEL-SCHUTTEN, APPLICANT: DIJKHUIZEN, LUBBEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 002018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 584
TYPE: PRT
ORGANISM: Leuconostoc mesenteroides
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ORGANISM: Lactobacillus reuteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                           167 IPNYSFVRAHDYDAQDPIRK 186
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Pred. No.
                                                                                                                                                                                                GERRITDINA HENDRIKA
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Pred. No.
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0.071;
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APPLICANT: KOSSMANN, Jens
APPLICANT: WELSH, Thomas
APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
FILE REFERENCE: 0147-0247P
CURRENT APPLICATION NUMBER: US/10/A17,280A
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: DE 19905069.4
PRIOR APPLICATION NUMBER: DE 19905069.4
PRIOR APPLICATION NUMBER: DE 19905069.4
PRIOR APPLICATION NUMBER: DE 19905069.4
PRIOR APPLICATION NUMBER: DE 19905069.4
PRIOR PILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
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NUMBER OF SEG ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEG ID NO 2
                                                                                                                                                                                                                                                                                                        Sequence 76653, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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SEQ ID NO 2
LENGTH: 2057
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                                                                                                                                                                                                                                 APPLICANT: Wang, I
APPLICANT: Zamudi
APPLICANT: Malone
APPLICANT: Haselt
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Best Local Similarity
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Lactobacillus reuteri
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                                                                                                                                                                                                                              Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                  Trawaccarr, Grant
Carr, Grant
Carr, Grant
Carr, Grant
                                                                                                                                                                                           Ohlsen, Kari
Zyskind, Judith
                                                                                                     Yamamoto, Ru
Forsyth, R.
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Pred. No. 0.
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; Sequence 44862, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
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US-10-425-114-44862
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 44862
LENGTH: 146
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SEQ ID NO 76653
LENGTH: 602
                                                                                                      Query Match
Best Local :
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 78614
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PRIOR PILLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-05-23
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ORGANISM: Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
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OTHER INFORMATION: Clone ID:
                                                                                                                                                                                                                                                      TYPE: PRT
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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                                                                                                      Similarity
                                       PNYVFIRAHDSEVQ 15
PSYVAVQKHESEVQ 14
                                                                                  Conservative
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                                                                                                      43.6%;
57.1%;
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56.2%; Pred. No. 17;
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                                                                                                      Score 48; DB 12; Length 146; Pred. No. 4.7;
                                                                                Mismatches
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RESULT 12

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RESULT 14
US-10-369-493-2894
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US-10-424-599-279743
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US-10-424-599-279743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB3227-021-C7_FLI.pep
US-10-425-114-61839
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Publication No. US/20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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SEQ ID NO 61839
LENGTH: 170
Sequence 2894, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
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Best Local (
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                                                                                                                                                                                                                                         Query Match
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabacka Tank
                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(251)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 251
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                                                                                                                                                                                                   Similarity 9; Conserv
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57.1%;
                                                                                                                                                                                                                      64.3%;
                                                                                                                                                                                                   Score 48; DB Pred. No. 8.8; Nismatches
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: HINTER: WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
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; ORGANISM: Thermotoga maritima
US-10-369-493-2894
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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SEQ ID NO 2894
LENGTH: 492
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Publication No. US20040029129A1
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Best Local Similarity
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APPLICANT:
APPLICANT:
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                                                                    PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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PRIOR APPLICATION NUMBER: 60/230,347
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Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                      FILING DATE:
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Trawick, John
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Pred. No.
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SEQ ID NO 47139 LENGTH: 506

TYPE: PRT ORGANISM: Borrelia burgdorferi

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                                                Query Match
Best Local Similarity
Thes 9; Conserv
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SEQ ID NO 64099
LENGTH: 557
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Publication No. US20040029129A1
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CURRENT FILING DATE: 2003-02-20
ERIOR APPLICATION NUMBER: 60/191,078
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TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207.727
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                                                                                                                                                TYPE: PRT
ORGANISM: Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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   463
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l Similarity 62.5%;
10; Conservative
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Malone, Cheryl
Haselbeck, Robert
IRIHDPEVQTRL 474
                                IRAHDSEVOTRI 18
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Zyskind, Judith
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                                                                 Conservative
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                                                                               42.7%;
                                                               Score 47; DB Pred. No. 33; 1; Mismatches
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Pred. No.
                                                                                DB 12;
33;
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; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP860
US-10-456-479-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rhodobacter sphaeroides US-10-369-493-8063
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US-10-369-493-8063
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Best Local Similarity 28.6%;
Matches 6; Conservative
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APPLICANT: Cao, You
APPLICANT: Hinkle,
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Publication No. US20030233675A1
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SEQ ID NO 8063
                                                                      Matches
                                                                                                      Query Match
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APPLICANT:
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PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: JP 2002-304232
PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 238700US0
CURRENT APPLICATION NUMBER: US/10/456,479
CURRENT FILING DATE: 2003-06-09
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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TYPE: PRT
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                                                                                       Local Similarity
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114 IPDYAYIVBYEGDVQSKVRSI 134
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                                 1 VPNYVFIRAHDSEVQTRIAKI 21
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: Slater, Steven C.
: Goldman, Barry S.
: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                           OKUDA, MITSUYOSHI
TAKIMURA, YASUSHI
SUMITOMO, NOBUYUKI
                                                                                                                                                                                                                                                                                                                                                                                                             NOMURA, MASAFUMI
KOBAYASHI, TOHRU
                                                                      Conservative
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                                                                                       40.9%; Score 45;
28.6%; Pred. No.
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Pred. No. 39;
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                                                                                     DB 12; Length 205; 22;
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RESULT 19 US-09-920-954-4 ; Sequence 4, Application US/09920954

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RESULT 21
US-10-389-566-1335
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                                                                                                                                                                                                                                               ; ORGANISM: Arabidopsis thaliana
US-09-758-269-2
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APPLICANT: SHIKATA, SHITSUW
APPLICANT: NOMURA, MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/920,954
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/509,814
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DCT/JP98/04528
PRIOR APPLICATION NUMBER: DT/JP98/04528
PRIOR APPLICATION NUMBER: JP98-10-07
PRIOR APPLICATION NUMBER: JP 9-274570
PRIOR APPLICATION NUMBER: JP 9-274570
PRIOR FILING DATE: 1997-06-08
PRIOR FILING DATE: 1997-06-08
                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 583
TYPE: PRT
                                                                                                                                                                                     Query Match
Best Local !
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Best Local Similarity
                                                                                                                                                                 Matches
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Patent No. US20020104120A1
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                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 2000-010056
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/758,269
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: JP 2001-003476
PRIOR FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IUCHI, SATOSHI
APPLICANT: KOBAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUO
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN TITLE OF INVENTION: CLEAVAGE ENZYME GENE FILE REFERENCE: 3914-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TAKAIWA, APPLICANT: OKUDA, I
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ORGANISM: Bacillus sp.
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                                                                                                                                                       40.0%; Score 44; DB 9; Local Similarity 42.1%; Pred. No. 1.1e+02; hes 8; Conservative 3: Miomorphis
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                                                                                  530 YIFCHVHDEETKTSELQII 548
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SAEKI, KATSUHISA
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HITOMI, JUN
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28.6%;
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PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR PRIOR PATEN 2002-06-26
PRIOR PILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOPTWARE: Patentin version 3.2
SEQ ID NO 1335
LENGTH: 727
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                                                                                                                                                                    ; ORGANISM: Physcomitrella patens US-10-389-566-2225
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; ORGANISM: Physcomitrella patens
US-10-389-566-1335
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 2225
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Publication No. US20040025202A1
GENERAL INFORMATION:
                                                                                   Matches
                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77 (52900) D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/365,301 PRIOR FILING DATE: 2002-03-15
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CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77 (52900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Monsanto Technology, LLC APPLICANT: Laurie, Cathy C
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                LENGTH: 727
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553 VPNOPHIRAHES-IMNRSAAMV 573
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                                     1 VPNYVFIRAHDSEVQTRIAKII 22
                                                                                 10; Conservative
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                                                                                                  45.5%;
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                                                                                 4; Mismatches
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Pred. No. 1.7e+02;
4; Mismatches 7;
                                                                                                     Score 43.5;
Pred. No. 1.
                                                                                                       .7e+02
                                                                                                                             DB 16;
                                                                                                                        Length
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US-10-282-122A-45816

Sequence 45816, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos

Malone,

Cheryl

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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45816
LENGTH: 297
TYPE: PRT
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Sequence 48707, Application US/10282122A publication No. US20040029129A1
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Best Local
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APPLICANT:
APPLICANT:
TITLE OF INVENTION: Identification of Essential Genes
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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PRIOR FILING DATE: 2000-03-21
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                                                                       APPLICANT:
                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                              APPLICANT: Wang,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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Malone, Cheryl
                                                                                                                                                                        Ohlsen, Kari
Zyskind, Judith
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Yamamoto, Robert
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Zyskind, Jud
                                                                                    Yamamoto, Rorsyth, R.
                                                                                                                       Carr, Grant
                                                                                                                                       Trawick, John
                                                                                                                                                          Wall, Daniel
                                                                                                                                                                                                             Haselbeck, Robert
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ilarity 41.2%;
Conservative
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                                                                                                          Robert
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                        in Microorganisms
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TITLE OF INVESTIGNAL Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT PLILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PRILING DATE: 2000-09-09
PRIOR PRILING DATE: 2000-09-09
PRIOR PRILING DATE: 2000-09-09
PRIOR PRILING DATE: 2000-09-09
PRIOR PRILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
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US-10-282-122A-55164
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Best Local Similarity 41.2%; Pred. No.
Matches 7; Conservative 5; Mismatc
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-02-16
Remetaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
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PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILLING DATE: 2001-02-09
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PRIOR APPLICATION NUMBER: 60/230,335
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PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
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FILING DATE:
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Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari
Zyskind, Judith
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US-10-369-493-17305
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
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SEQ ID NO 17305
LENGTH: 144
TYPE: PRT
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55164
LENGTH: 457
                                                                                                    APPLICANT: Wang,
APPLICANT: Zamud
APPLICANT: Malon
APPLICANT: Hasel
APPLICANT: Ohlse
                                                                                                                                                                                                              Sequence 56323, Application US/10282122A
Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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nes 9; Conserv
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                                                                    Ohlsen, Kari
Zyskind, Jud
Wall, Daniel
Foreyth, R.
                                                                                                                        Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                   Trawick, John
                                  Carr, Grant
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lio, Carlos
                                                                    Daniel
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                 Robert
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Pred. No. 1.2e+02;
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Pred. No.
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PRIOR PILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323) B
FULE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 194106
LENGTH: 963
Query Match
Best Local Similarity %0...
Thes 7; Conservative
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 56323
LENGTH: 484
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Best Local
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                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(963)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_17303C.1.pep
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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FILING DATE: 2000-11-27
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                                                       38.2%;
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23.8%; Pred. No. 1.90
tive 10; Mismatches
                                   Score 42; DB 12;
Pred. No. 4.3e+02;
2; Mismatches 6
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RESULT 29
US-09-864-761-41675
; Sequence 41675, Application
; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
FEATURE:

OTHER INFORMATION: EXPRESSE
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                   LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/234,687
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APPLICANT: Regents of the University of California
APPLICANT: Gerald, NEWTON
APPLICANT: Av-Gay, YOSSEF
APPLICANT: Robert, FAHEY
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    28-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 14; 49pp; English.
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                                                          AAR32925 standard; protein; 1592
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722
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100.0%; Pred. No. 1.9e-09;
tive 0; Mismatches 0;
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Matches 22; Conser
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(FUKU/) FUKUI I.
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Anti-caries agent composed of a monoclonal antibody against an inhibitory

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                                                       The invention relates to a monoclonal antibody against dental caries and an anti-caries agent composed of a monoclonal antibody produced by Streptococcus mutans, particularly mouse-hybridoma MHP126 (FERM P-17567), against an enzyme having inhibitive activity against water insoluble glucan synthetase of glucosyl transferase-B. The monoclonal antibody specifically inhibits water insoluble glucan synthetase of Streptococcus mutans produced glucosyl transferase-B and is used in the immunotherapy of dental caries. This sequence represents a Streptococcus mutans monoclonal antibody-related
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The invention an isolated protein comprising a glucosyltransferase (GTF) CC Hoppeptide having changes at position from 1748V, D457N, D567T, D457N/D571K, D567T/D571K, D567T/D571K, K1014T, CC (14487, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K, K1014T, CC (1470)D457N/D567T, D571K/K1014T, CC (1471)D457N)D567T, D571K/K1014T, CC (1471)D457N)D567T, D571K/K1014T, CC (1471)D4589D, and N471D/T589D. Also included are a glucan produced by the CC (GTF mutant, an isolated polymucleotide which encodes Pl or P2, or its complementary polymucleotide, a ribonucleic acid sequence encoding the CC (GTF mutant, an expression cassette comprising the polymucleotide operably CC (Inked to a promoter, a vector, a transgenic plant; a paper sizing and/or vector, a seed or tuber from the transgenic plant; a paper sizing and/or coating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTF, wild type or, starch, a latex, the squeam produced in starch biosynthesis, transformed with a gene encoding a glucan produced in the amyloplast and/or vacuole or a maize line comprising the glucan in starch biosynthesis, transformed with a gene encoding a comprising the glucan producing a glucan in a plant. The vector is useful for producing a glucan in a plant. The method comprises transforming a plant cell with the vector, growing the plant cell under plant growing a plant.
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Matches 20
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16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. mutans glucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 30-33; 44pp;
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Pred. No. 2.7e-08;
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                                                                The invention relates to a monoclonal antibody against dental caries and an anti-caries agent composed of a monoclonal antibody produced by Streptococcus mutans, particularly mouse-hybridoma MHP126 (FERM P-17566) or mouse-hybridoma MHP136 (FERM P-17567), against an enzyme having inhibitive activity against water insoluble glucan synthetase of glucosyitransferase-B. The monoclonal antibody specifically inhibits water insoluble glucan synthetase of Streptococcus mutans produced glucosyltransferase-B and is used in the immunotherapy of dental caries. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotide for a time sufficient to produce the glucan in the regenerated plant, where the vector contains a transit sequence from ribulose biphosphate carboxylase small subunit, waxy, brittle-1 and chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. Glucans are useful as substitutes for and additions to modified starch and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present
Sequence
                                                                                                                                                                                                                                                          Anti-caries agent composed of a monoclonal antibody against an inhibitory enzyme against water insoluble glucan synthetase of glucosyl transferase-B (GTP-B) of Streptococcus mutans.
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                                                  sequence
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 1375
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                                                  represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dental caries; water insoluble glucan synthetase; anti-caries;
                                                                                                                                                                                                                                                         of Streptococcus mutans
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 AA;
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86.4%;
                                                  Streptococcus
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Pred. No.
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                                                     mutane
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                                                   monoclonal antibody-related
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Query Match

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Length 1375;

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RESULT 7
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                                                                                                                                                                                                                                The present sequence is the protein sequence of Streptococcus mutans glucosyltransferase-C (GTF-C). Peptide fragments of GTF-C, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II protein-binding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                           Sequence 1375
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 13; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2003; 2003WO-US006962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus mutans glucosyltransferase-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD93655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD93655 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-845091/78.
                                     AAU98031
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                                                                                                                                                         19;
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPSYSFIRAHDSEVQDLIRNII 599
                                                                                                        VPSYSFIRAHDSEVQDLIRNII 599
                                                                                                                     VPSYSFARAHDSEVQDIIRDII 22
                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taubman
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                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                     protein;
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                                                                                                                                                                     89.1%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme; vaccine; anticaries; epitope;
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                                                                                                                                                                       Score 98;
Pred. No.
                                                                                                                                                          Mismatches
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                                        ΑA
                                                                                                                                                                        .Be-07;
                                                                                                                                                                                   Length 1375;
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in immunogenic
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27-AUG-2002

(first

entry)

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CC GIF mutant, an expression cassette comprising the polynucleotide operably collinked to a promoter, a vector comprising the polynucleotide operably collinked to a promoter, a vector, a transgenic plant comprising the comprising the comprising the comprising the expression cassette, host colling to tuber from the transgenic plant, a paper sizing and/or coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GIF, wild type or, starch, a latex, thermoplastic molecule or their combinations or glucan and starch where the glucan is produced in the amyloplast and/or vacuole or a maize line comprising the glucan (paper sizing/coating agent). The vector is useful for producing a glucan in a plant. The method comprises transforming a comprising the glucan in a plant. The method comprises transforming a conditions to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the composerated plant, where the vector contains a transit sequence from continuous biphosphate carboxylase small subunit, waxy, brittle-1 and chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet.

CC Glucans are useful as substitutes for and additions to modified starch conditions to maintacture. Unlike prior art techniques, which creative input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T/D571K, M790, M567T/D57K/K779Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T599E, N471D, M471D/T589D, and N471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polymicalectide which encodes P1 or P2, or its complementary polymicalectide, a ribonucleic acid sequence encoding the GTF mutant, an expression cassette comprising the nolymicalectide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
11-DEC-1998;
The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K/K1014T, I448V/D457N/D567T/D571K/K779Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T599E, N471D, N471D/T589E, Also included are a glucan produced by the GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       properties and impart gloss to the paper during coating step. The present sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1475
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                                                                                                                                                                                                                                                                                                            Glucosyltransferase B or D protein useful as substitutes for and additions to modifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glucosyltransferase;

    mutans glucosyltransferase GTFB mutant

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                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-414332/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coating composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NICH/) NICHOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                 36; Page; 44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vacuole;
                                                                                                                                                                                                                                                                                  comprises mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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95US-00482711.
95US-00485243.
98US-00007999.
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98US-00009620.
98US-00210361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paper
                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Wild-type Lys substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  manufacture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 97;
Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                             in useful for producing
to modified starch and
in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9e-07;
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                                                                                                                                                                                                                                                                                                               a glucan useful
latexes in pape
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coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, combinating composition molecule or their combinations or glucan and starch where the glucan is produced in the amyloplast and/or vacuole or a maize line deficient in starch biosynthesis, transformed with a gene encoding a glucosyltransferase B or D enzyme, wild-type or mutant and a paper comprising the glucan (paper sizing/coating agent). The vector is useful for producing a glucan in a plant. The method comprises transforming a glunt cell with the vector, growing the plant growing conditions to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the regenerated plant, where the vector formatins a transit sequence from craylong phylography protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. CG Glucans are useful as substitutes for and additions to modified starch can latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce day GTF, which utilises chiologically produced input materials, is more cost-effective and convironmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coating step. The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                 07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linked to a promoter, a vector comprising the expression cassette, must cell introduced with the vector, a transgenic plant comprising the vector, a seed or tuber from the transgenic plant, a paper sing and/or vector, a seed or tuber from the transgenic plant, a paper sing and/or vector, a seed or tuber from the transgenic plant, a paper sing and/or vector, a seed or tuber from the transgenic plant, a paper sing and/or vector, a seed or tuber from the transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                      Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. mutans glucosyltransferase GTFB mutant K1014T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU98033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU98033 standard; protein; 1475 AA
                                                                                                      19-DEC-2000;
                                                                                                                                               14-MAR-2002
                                                                                                                                                                                   US2002031826-A1
                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                       amyloplast; vacuole;
                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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19; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an expression cassette comprising the polynucleotide operably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                      2000US-00740274.
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                                                                                                                                                                                                                                                                                                                                 mutans
95US-00478704.
95US-00482711.
95US-00485243.
98US-00007999.
                                                                                                                                                                                                                                             Location/Qualifiers 1014
                                                                                                                                                                                                                            /note= "Wild-type Lys substituted by Thr"
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                                                                                                                                                                                                                                                                                                                                                                       paper manufacture; mutant; mutein.
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Pred. No. 2.9e-07;
1; Mismatches 2;
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RESULT 11 AAU98030

AAU98030 standard;

protein; 1475

A

27-AUG-2002 AAU98030;

(first entry)

맑 á

552 VPSYSFIRAHDSEVODLIADII 573

VPSYSFARAHDSEVQDIIRDII 22

Matches Query Match Best Local

19; Н

Conservative

1; Mismatches Score 97; I Pred. No. 2.

<u>ب</u>

0;

Gaps

0

Local

Similarity

88.2%;

B .9e-07 υı

Length 1475; Indels

Sequence 1475

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comprementary polymucleotide, a ribonucleic acid sequence encoding the cell introduced with the vector comprising the polymucleotide operably cell inked to a promoter, a vector comprising the expression cassette, host cell introduced with the vector, a transgenic plant comprising the vector, as seed or tuber from the transgenic plant comprising the coating composition comprising a glucan produced in a paper sizing and/or coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, comprising the glucan is produced in the amyloplast and/or vacuole or a maize line deficient in starch biosynthesis, transformed with a gene encoding a comprising the glucan (paper sizing/coating agene encoding a comprising the glucan in a plant. The method comprises transforming a plant cell with the vector, growing the plant cell under plant growing conditions to produce a regenerated plant and inducing expression of the polymucleotide for a time sufficient to produce the glucan in the regenerated plant, where the vector of the produce the glucan in the produced in the amyloplast of potato or the vacuole of sugar beet. Cell comparison to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. Cell comparison to produce the glucan plant, and glucan cell value in paper manufacture. Unlike prior art techniques, which cell manufacture utilising the glucan produce displaced in for any additions to modified starch cell withing the glucan produced of growing the paper during coating step. The present sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the glucar in a paper during coating step. The present considered by the indexer in paper manufacture and specification but was created by the indexer using the glucan in the scenarior as axingancy and the information in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from 1448V, D457N, D567T, M457N/D57T, D457N/D57TK, D567T/D571K/K1014T, K1014T, M457N/D567T, D457N/D57TK, D567T/D57TK, D567T/D57TK/K1014T, T1448V/0457N/D567T/D57TK/K779Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D, N471D/T589D, and M471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in paper manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                        the GTFB sequence appearing as AAU98027 and the information 36\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Page; 44pp; English.
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98US-00009620.
98US-00210361.
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The invention an isolated protein comprising a glucosyltransferase (GTF) CC B polypeptide having changes at position from 1448V, D457N, D567T, D457N/D567T, D457N/D571K, D567T/D571K, D567T, D571K, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T, D667T
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
The invention an isolated protein comprising a glucosyltransferase (GTF) B polypeptide having changes at position from I448V, D457N, D567T, D457N/D567T, D457N/D571K, D567T,D571K, D567T,D571K, D567T,D571K/K1014T, I69A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D, T589E, N471D/T589D, and N471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the GTF mutant, an expression cassette comprising the polynucleotide operably
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Synthetic.
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linked to a promoter, a vector comprising the expression cassette, host cell introduced with the vector, a transgenic plant comprising the vector, a seed or tuber from the transgenic plant, a paper sizing and/or coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, thermoplastic molecule or their combinations or glucan and starch where the glucan is produced in the amyloplast and/or vacuole or a maize line

Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in paper manufacture, comprises mutations in specific positions.

N-PSDB; ABK52938

WPI; 2002-414332/44.

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deficient in starch biosynthesis, transformed with a gene encoding a CC glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC comprising the glucan (paper sizing/coating agent). The vector is useful CC for producing a glucan in a plant. The method comprises transforming a CC plant cell with the vector, growing the plant cell under plant growing conditions to produce a regenerated plant and inducing expression of the CC polynucleotide for a time sufficient to produce the glucan in the polynucleotide for a time sufficient to produce the glucan in the CC regenerated plant, where the vector contains a transit sequence from CC ribulose biphosphate carboxylase small subunit, waxy, brittle-1 and CC conditions to the manufacture to produce the vacuole of sugar beet. CC glucans are useful as substitutes for and additions to modified starch CC and latexes in paper manufacture. Unlike prior art techniques, which crequire input materials and produced chemical effluents, paper CC require input materials that produce chemical effluents, paper CC inclogically produced input materials, is more cost-effective and CC environmentally friendly. Moreover, glucans also exhibit thermoplastic groperties and impart gloss to the paper during coating step. The present sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer in the information in
THE SECRET SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF 
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Best Local
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07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amyloplast; vacuole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coating composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. mutans glucosyltransferase GTFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                     19-DEC-2000;
                                                                                                                              16-JAN-1998
20-JAN-1998
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                              (NICH/)
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                                     NICHOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                         2000US-00740274.
                                                                                                                           95US-00478704.
95US-00482711.
95US-00485243.
95US-00007999
98US-00008172.
98US-00009620.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTFB; transgenic plant; paper sizing; glucan; starch; latex; thermoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  paper manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 97; DB 5;
Pred. No. 2.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Sequence 1475 AA;

sequence represents GTFB

properties and impart gloss to the paper during coating step.

The present

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CC B polypeptide having changes at position from 1448V, 0457N, D557T, D457N/D57TK, D457N/D57TK, D567T/D57TK/X014T, CC K1014T, D457N/D57TK, D457N/D57TK, D567T/D57TK/X014T, CC 1448V/D457N/D57TK/X014T, D567T/D57TK/X014T, CC GTF D polypeptide having changes at positions from T589B, And K779Q or a CC GTF D polypeptide having changes at positions from T589B, T589B, N471D, CC GTF mutant, an expression cassette comprising the expression produced by the CC GTF mutant, an expression cassette comprising the polynucleotide operably CC GTF mutant, an expression cassette comprising the polynucleotide operably CC GTF mutant, an expression cassette comprising the polynucleotide operably CC GTF mutant, an expression cassette comprising the polynucleotide operably CC GTF mutant, an expression cassette comprising the polynucleotide operably CC GTF mutant, an expression cassette comprising the polynucleotide operably CC GTF mutant, an expression cassette comprising the polynucleotide operably CC GTF mutant, an expression cassette, host CC GTF mutant, an expression comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, CC where the following a glucan produced in the amyloplast and/or vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a CC comprising the glucan (paper sizing/coating agent). The vector is useful comprising the glucan format and apper scale of the produce and paper sizing comprising transforming a cC comprising the plant call with the vector format and inducing expression of the CC conditions to produce a transforming a plant comprising the plant and inducing expression of the conditions to produce a transforming a plant call with the vector small subunit, waxy, brittle-1 and cC is produced in the amyloplast of potato or the vacuole of sugar beet. CC conditions to modified starch conditions to modified starch conditions to modified starch conditions to modified starch conditions to modified starch conditions to 
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RESULT 14
ADD93654
ID ADD93
XX
AC ADD93
XX
AC ADD93
XX
XX
E---XX
XX
C---XX
XX
Glucc
XX
XX
Strep
XX
MO200 片 Query Match Best Local Matches Streptococcus mutans glucosyltransferase-B ADD93654; ADD93654 standard; protein; 1475 29-JAN-2004 (first entry 552 VPSYSFIRAHDSEVQDLIADII 573 19; 1 VPSYSFARAHDSEVQDIIRDII 22 Similarity Conservative 88.2%; Mismatches Score 97; Pred. No. DB 5; Length 1475; .9e-07; ,. N Indels 0 Gaps 0

Glucosyltransferase; enzyme; vaccine; anticaries; epitope; immunogen

WO2003075845-A2

Streptococcus mutans

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AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC XXX AC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition useful as vaccines for a glucan binding protein-B binding class II protein.
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08-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1475 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2003; 2003WO-US006962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. mutans glucosyltransferase GTFB mutant D457N/D571K
                                                                                       14-MAR-2002
                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU98035 standard; protein; 1475 AA
                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                               US2002031826-A1
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2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                       571
                                                                                                                                                                                                          /note= "Wild-type Asp
                                                                                                                                                                                                                                                                   note= "Wild-type Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 97; DB
Pred. No. 2.9e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
2.9e-07;
                                                                                                                                                                                                          substituted by Lys'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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19-DEC-2000; 2000US-00740274

RESULT 16
AAU98034
ID AAU98034 standard; protein; 1475 AA

S 片

1 VPSYSFARAHDSEVQDIIRDII 22 VPSYSFIRAHDSEVQDLIAKII 573

Matches

18;

Conservative

Query Match Best Local Similarity

81.8%;

Score 90; Pred. No. 1; Mismatches 4. DB 5; .5e-06;

Length 1475; Indels

0

0

Sequence 1475 AA;

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Comptementary polynucies or a ribonucies acta sequence encoding the coll introduced with the vector comprising the polynucleotide operably cell introduced with the vector, a transgenic plant comprising the vector, a seed or tuber from the transgenic plant comprising the coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, cell through a plucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, cell with a gene encoding the mutant GTF, wild type or, starch, a latex, cell with a gene encoding the mutant GTF, wild type or starch, a latex, cell with a gene encoding a glucan produced in the amyloplast and/or vacuole or a maize line deficient in starch biosynthesis, transformed with a gene encoding a glucan cell with the vector, growing the plant and a paper of plant feell with the vector, growing the plant cell under plant growing conditions to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the regenerated plant, where the vector contains a transit sequence from cell under plant and substitutes for and additions to modified starch is produced in the amyloplast of potato or the vacuole of sugar beet. Cell canns are useful as substitutes for and additions to modified starch and latexes in paper manufacture. Unlike prior art techniques, which cell withless that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically friendly. Moreover, glucans also exhibit thermoplastic environmentally friendly. Moreover, glucans also exhibit thermoplastic sequence represents a GTFB mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer middle sequence is not shown in the specification sequence in formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
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07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glucosyltransferase B or D protein useful for producing a glucan useful as substitutes for and additions to modified starch and latexes in paper manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention an isolated protein comprising a glucosyltransferase B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D571K, D567T/D571K, D567T/D571K, D567T/D571K/K1014T, X169A/Y171A, AND K779Q 1448V,D457N/D567T/D571K/K779Q/K1014T, X169A/Y170A/Y171A, and K779Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 36; Page; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-414332/44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NICH/) NICHOLS
                                                                                   the GTFB
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95US-00482711.
95US-00485243.
                                                                              sequence appearing as AAU98027 and the information
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98US-00009620.
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CC The invention an isolated protein comprising a glucosyltransferase (GTP) CC B polypeptide having changes at position from 1448V, D457N, D567T, D457N/D571K, D567T/D571K, D567T/D571K, N1567T, D577T/S71K/X1014T, CC I1448V/D457N/D567T, D457N/D571K, D567T/D571K, X1014T, CC II448V/D457N/D567TD, T589E, Also included are a glucan produced by the CC GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its complementary polynucleotide, a ribonucleic acid sequence encoding the complementary polynucleotide, a ribonucleic acid sequence encoding the vector, a promoter, a vector comprising the polynucleotide operably clinked to a promoter, a vector comprising the pant comprising the vector, a seed or tuber from the transgenic plant, a paper sizing and/or coating composition comprising a glucan produced in a plant transformed with a gene encoding the mutant GTF, wild type or, starch, a latex, the glucan is produced in the amyloplast and/or vacuole or a maize line deficient in starch biosynthesis, transformed with a gene encoding a glucan (paper sizing/coating agent). The vector is useful for producing a glucan in a plant. The method comprises transforming a glucosyltransferase B or D enzyme, wild-type or mutant and a paper comprising the vector, growing the plant cell under plant growing a plant cell with the vector is useful for producing a glucan in a plant. The method comprises transforming a conditions to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the regenerated plant, where the vector contains a transit sequence from chorometals binding expression of the polynucleotide in the amyloplast of potato or the vacuole of sugar beet. is produced in the amyloplast of potato or the vacuole of sugar beet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amyloplast; vacuole; paper manufacture; mutant; mutein.
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 36; Page; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NICH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutans glucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    composition;
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95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
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thermoplastic
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latexes in pape
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paper

The invention an isolated protein comprising a glucosyltransferase B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D571K, D567T/D571K, 7T/D57TK, D567T/D57TK, D567TK,

Claim 36; manufacture,

Page; 44pp;

English

as substitutes for and additions

or D protein useful for producing dadditions to modified starch and mutations in specific positions.

latexes

glucan useful

ij

(GTF)

comprises mutations

Glucosyltransferase B

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glucans are useful as substitutes for and additions to modified starch and latexes in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper manufacture utilising the glucan produced by GTF, which utilises biologically produced input materials, is more cost-effective and environmentally friendly. Moreover, glucans also exhibit thermoplastic properties and impart gloss to the paper during coatting step. The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in claim 36
                                                                                                                                                                                   07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein.
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                                                                                                         WPI; 2002-414332/44.
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95US-00482711.
95US-00485243.
95US-00007999.
98US-00008172.
98US-00009620.
98US-00210361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 1475
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81.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTFB mutant D567T.
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4.5e-06;
- 3;
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I448V/D457N/D567T/D571K/K779Q/K1014T, Y169A/Y170A/Y171A, and K779Q or a GTF D polypeptide having changes at positions from T589D, T589E, N471D/T589D, and N471D/T589E. Also included are a glucan produced by the GTF mutant, an isolated polynucleotide which encodes P1 or P2, or its

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ID ABR63235
XX ABR63236
AC ABR63
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DT 23-OC
DT 27-AL
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                                                                     20-JUL-2001;
25-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                           Lactobacillus sakei
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                                                                         2001EP-00202752.
2001EP-00202841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence from strain KG15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 90; DB ; Pred. No. 4.5e 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACC84451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2055 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2001; 2001EP-00202752.
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glucan; glucosyltransferase activity; thickener; preblotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucansucrase sequence from strain Lb33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR63236 standard; protein; 1149
                                                                                                                                                  Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of all (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003008618-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactobacillus fermentum.
                                                                                          Claim 11; Fig 1; 51pp; English
                                                                                                                                                                                                                                                                                                                    WPI; 2003-289780/28.
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                                                                                                                                                                     consisting of alpha
useful as thickener.
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The present invention relates to glucan capable of being glucosyltransferase activity of a lactic acid bacterium o

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU98036 standard; protein; 1475 AA
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  The invention an isolated protein comprising a glucosyltransferase B polypeptide having changes at position from I448V, D457N, D567T, K1014T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K, L1014T, V169A/Y170A/Y171A, and K779Q
                                                                                                                                                                                Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                             WPI; 2002-414332/44.
                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                     36; Page;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composition;
                                                                                                                                                                                                                                                                                                                                                                                                  NICHOLS
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98US-00007999.
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95US-00482711.
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                                                                                                                                  44pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Wild-type Asp substituted
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTFB; transgenic plant; paper sizing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucan; starch; latex; thermoplastic molecule;
                                                                                                                                     English
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Pred. No.
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latexes in pape
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RESULT 21
AAU98037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC GTF D polypeptide having changes at positions from T589D, T589E, N471D, CC GTF matant, an isolated polynucleotide which encodes P1 or P2, or its C complementary polynucleotide, a ribonucleic acid sequence encoding the CC complementary polynucleotide, a ribonucleic acid sequence encoding the CC complementary polynucleotide, a ribonucleic acid sequence encoding the CC complementary polynucleotide operably CC linked to a promoter, a vector comprising the sypression cassette, host CC vector, a seed or tuber from the transgenic plant, a paper sixing and/or coating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTE, wild type or, starch, a latex, the glucan is produced in the amyloplast and/or vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a CC deficient in starch biosynthesis, transformed with a gene encoding a CC deficient in starch biosynthesis, transformed with a gene encoding a CC comprising the glucan (paper sixing/coating agent). The vector is useful comprising the glucan in a plant. The method comprises transforming a CC for producing a glucan in a plant. The method comprises transforming a CC plant cell with the vector, growing the plant cell under plant growing the plant cell under plant growing cC conditions to produce a regenerated plant and inducing expression of the regenerated plant, where the vector contains a transgenic plant, and glucan cc is produced in the amyloplast of potato or the vacuole of sugar beet. CC dlucans are useful as substitutes for and additions to modified starch cC and latexes in paper manufacture. Unlike prior art techniques, which cc graphire imput materials that produce a transgenic plant, and glucan cc are guitant produced in the appear and additions to modified starch cc graphic ture to produce themical efficients, paper conditied starch cc graphic produced in the prosent cc graphic produced in the prosent cc graphic produced in the produced produced by CTF, which utilises bi
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Matches
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Best Local &
                                                                                                                                                                                                                                                       Glucosyltransferase; GTFB; transgenic plant; paper sizing; coating composition; glucan; starch; latex; thermoplastic molecule; amyloplast; vacuole; paper manufacture; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                      Streptococcus mutans Synthetic.
                                                                                                                                                                                                                                                                                                                                      S. mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAU98037;
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                                                                                                            Misc-difference
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                                                                                                                                 "Wild-type Asp
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Pred. No.
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1014

/note= /note=

"Wild-type Lys

Bubstituted

Ϋ́ by Lys"

Thr"

"Wild-type Asp

<u>aubstituted</u>

19-DEC-2000; 14-MAR-2002

2000US-00740274

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complementary polynucleotide, a ribonucleit add sequence encoding the CC GTF mutant, an expression cassette comprising the polynucleotide operably CC linked to a promoter, a vector comprising the expression cassette, host CC cell introduced with the vector, a transgenic plant comprising the CC vector, a seed or tuber from the transgenic plant, a paper sizing and/or CC coating composition comprising a glucan produced in a plant transformed CC with a gene encoding the mutant GTF, wild type or, starch, a latex, CC thermoplastic molecule or their combinations or glucan and starch where CC the glucan is produced in the amyloplast and/or vacuole or a maize line CC deficient in starch biosynthesis, transformed with a gene encoding a CC glucosyltransferase B or D enzyme, wild-type or mutant and a paper CC comprising a glucan (paper sizing/coating agent). The vector is useful CC for producing a glucan in a plant. The method comprises transforming a CC plant cell with the vector, growing the plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the cc regenerated plant, where the vector contains a transit sequence from cc chlorophyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. CC glucans are useful as substitutes for and additions to modified starch cc and latexes in paper manufacture. Unlike prior art techniques, which cc comprises and impart gloss to the paper during coating step. The present CC sequence is not shown in the specification but was created by the indexer cusing the GTFB sequence appearing as AAU98027 and the information in
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Matches
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20-JAN-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucosyltransferase B or D protein useful for producing as substitutes for and additions to modified starch and manufacture, comprises mutations in specific positions.
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07-JUN-1995;
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77.3%;
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The invention an isolated protein comprising a glucosyltransferase (GTF) CC B polypeptide having changes at position from I448V, D457N, D567T, CC K1014T, D457N/D567T, D457N/D571K, D567T/D571K, D567T/D571K, D567T/D571K, M567T/D571K,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
16-JAN-1998;
16-JAN-1998;
20-JAN-1998;
11-DEC-1998;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     λĄ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thr!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a glucan useful
latexes in pape:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paper
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RESULT 23
ABR63228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the glucan is produced in the amyloplast and/or vacuole or a maize line condicient in starch biosynthesis, transformed with a gene encoding a glucosyltransferase B or D enzyme, wild-type or mutant and a paper comprising the glucan (paper sizing/coating agent). The vector is useful comprising the glucan in a plant. The method comprises transforming a complex conditions to produce a regenerated plant and inducing expression of the polynucleotide for a time sufficient to produce the glucan in the coll with where the vector contains a transit sequence from continuous biphosphate carboxylase small subunit, waxy, brittle-1 and controphyll AB binding protein to produce a transgenic plant, and glucan is produced in the amyloplast of potato or the vacuole of sugar beet. Contains are useful as substitutes for and additions to modified starch cardiateses in paper manufacture. Unlike prior art techniques, which require input materials that produce chemical effluents, paper convironmentally friendly. Moreover, glucans also exhibit thermoplastic proporties and impart gloss to the paper during coating step. The present sequence is not shown in the specification but was created by the indexer using the GTFB sequence appearing as AAU98027 and the information in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucansucrase sequence from strain Lb86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR63228 standard;
                                                                                                                  WPI; 2003-289780/28.
N-PSDB; ACC50072.
                                                                                                                                                                                                                                                                                                                    20-JUL-2001; 2001EP-00202752.
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucan; glucosyltransferase activity; thickener; poioactive agent; anti-corrosion agent; foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-2003
Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener.
                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-2002; 2002WO-NL000495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003008618-A2
                                                                                                                                                                                                          Geel- Schutten GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VPSYSFARAHDSEVQDIIRDII 22
                                                                                                                                                                                                                                                                      NEDERLANDSE ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPSYSFIRAHDSEVOTLIAKII 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%;
77.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ጅ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prebiotic;
; gastrointestinal tract
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The present invention relates to glucan capable

of.

being

produced

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Matches Query Match Best Local S

L Similarity

Conservative

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73.6%; 71.4%;

Score 81; Pred. No. (

0.00016;

Length 1499; Indels

0;

Gaps

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Sequence 1499

AA,

Claim 11; Page 27; 51pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bloactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the castrointestinal tract. The present sequence represents a sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    giucansucrase gene
                               This invention relates to a modified dextran sucrase (DS) exchanging one site of the active centre zone of a dextran sucrase for the active centre zone of different types of dextran sucrase. Glucan is a polysaccharide (for example dextran) which uses D-glucoses, such as a starch and a cellulose, as a structural unit. The modified enzyme of the invention is useful in the manufacture of glucan. The selection of the active centre area of DS which carries out transduction, enables changes in structure and character of an enzyme-reaction product and their application to various uses. The present sequence is that of a protein which is related to the Leuconostoc mesenteroides dextran sucrase protein and which was used during the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dextran sucrase; active centre zone; D-glucose; starch; cellulose; glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP2003111590-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme-reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC54806 standard; protein; 1499
                                                                                                                                                                                                                                                                                    Novel modified dextran sucrase which exchanges one site of active center zone of dextran sucrase for active center zone of different types of dextran sucrase, useful for manufacturing glucan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2001; 2001JP-00307067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2001; 2001JP-00307067.
                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 11; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ADC54814.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-735670/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                  (DOKU-) DOKURITSU GYOSEI HOJIN SHOKUHIN SOGO KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 IPNÝŠEVRÁHDŠEVQTVIAQII 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VPSYSFARAHDSEVQDIIRDII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq ID11 related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%;
68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L mesenteroides dextran sucrase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82; DB 6;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucan; polymaccharide; dextran; manufacture; transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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RESULT 25
AAU80055
ID AAU80
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                                                                                                                                           The invention relates to preparation of a fermented food product that concludes treating the microorganism (A) to be used for fermentation with a dextransucrase so that this binds to the cell walls of (A). The method is used to produce yoghurt, curd, cheese or other fermented milk confight formulae and pet foods. Dextransucrase can also be bound to e.g. crimins or oral vaccines for delivering these to foods, using (A) as concarrier. The method produces foods with attractive and uniform texture, since dextransucrase is evenly distributed and forms a thickening agent consistent with the amount formed being controlled by the amount of certical cardieve a good texture, so the amount of becaused. Dextransucrase bound, Milk does not have to be coagulated in order to reduced. Dextransucrase binds to many different types of cells over wide cranges of temperature and plh and the treated bacteria can be stored in controlled or powdered form. The present sequence represents the amino acid gequence of dextransucrase
                                                           Matches
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1201131-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leuconostoc mesenteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dextransucrase; yoghurt; curd; cheese; fermented milk; infant formulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU80055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU80055 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparing fermented food products, e.g. yoghurt, using microorganisms that have dextran sucrase bound to the surface, provide attractive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pet food; vitamin;
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14-20; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         uniform texture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-373873/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bauche A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-2000; 2000EP-00123012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-2000; 2000EP-00123012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leuconostoc mesenteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEST
                                                                                                                  Sequence 1527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625
652 IPNYSTVRAHDSEVOTVIAQIV 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSYSFARAHDSEVQDIIRDII
                         VPSYSFARAHDSEVQDIIRDII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Maleprade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROD NESTLE SA.
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oral vaccine; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 1527 AA
                                                                       73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dextransucrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duboc P,
                                                         Score 81; DB
Pred. No. 0:00
4; Mismatches
                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neubauer H,
                                                                           DB 5;
0.00017;
                                                              4
                                                                                         Length 1527;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zink
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                                                                Gaps
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RESULT 26 ADC54807 ID ADC54

ADC54807 standard; protein; 1527

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18-SEP-2003 WO2003075845-A2

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RESULT 27
ADD93658
ID ADD93
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                                                                                                                                                                                                                                                                                                             S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a modified dextran sucrase (DS) exchanging one site of the active centre zone of a dextran sucrase for the active centre zone of different types of dextran sucrase. Glucan is a polysaccharide (for example dextran) which uses D-glucoses, such as a starch and a cellulose, as a structural unit. The modified enzyme of the invention is useful in the manufacture of glucan. The selection of the active centre area of DS which carries out transduction, enables changes in structure and character of an enzyme-reaction product and their application to various uses. The present sequence is that of the Leuconostoc mesenteroides dextran sucrase protein used during the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2003111590-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dextran sucrase; active centre zone; glucan; polysaccharide; dextran; D-glucose; starch; cellulose; glucan manufacture; transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2001; 2001JP-00307067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leuconostoc mesenteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC54807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel modified dextran sucrase which exchanges one site of active center zone of dextran sucrase for active center zone of different types of dextran sucrase, useful for manufacturing glucan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2001; 2001JP-00307067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADC54802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DOKU-) DOKURITSU GYOSEI HOJIN SHOKUHIN SOGO KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 12; 28pp; Japanеве.
                                                                                              Glucosyltransferase; enzyme; vaccine; anticaries; epitope; immunogen
                                                                                                                           Streptococcus sobrinus glucosyltransferase-U.
                                                                                                                                                     29-JAN-2004
                                                                                                                                                                                                              ADD93658 standard; protein; 1554
                                                                     Streptococcus
                                                                                                                                                                                   ADD93658;
                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-735670/70.
                                                                                                                                                                                                                                                                                                                                           l Similarity
                                                                                                                                                                                                                                                                                                    1 VPSYSFARAHDSEVQDIIRDII 22 :|:||| ||||||| :| |:
                                                                                                                                                                                                                                                                                      IPNYSFVRAHDSEVQTVIAQIV 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mesenteroides dextran sucrase protein
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                           73.6%;
                                                                                                                                                                                                                                                                                                                                            Score 81; DB 7;
Pred. No. 0.00017;
4; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                            Length 1527;
                                                                                                                                                                                                                                                                                                                                                 Indels
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RESULT 28
ABR63229
ID ABR63
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Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glucosyltransferase-U (GTF-U). Peptide fragments of GTF-U, especially from the catalytic domain of the polypeptide, can be used in immunogenic compositions and subunit vaccines for dental caries. These compositions comprise a major histocompatibility complex (MHC) class II protein-binding peptide from S. mutants glucan binding protein-B (GbpB) covalently linked with a peptide fragment of a streptococcal glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 15; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-845091/78.
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08-AUG-2002;
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Novel glucan produced by glucosyltransferase activity of lactic
                                                                                                                                                                                                                                                                      Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
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                                                                                                                      20-JUL-2001; 2001EP-00202752.
25-JUL-2001; 2001EP-00202841.
                                                                                                                                                              22-JUL-2002; 2002WO-NL000495
                                                                                                                                                                                         30-JAN-2003
                                                                                                                                                                                                                    WO2003008618-A2
                                                                                                                                                                                                                                             Leuconostoc
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                                                                                              (NEDE ) NEDERLANDSE ORG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is the protein sequence of Streptococcus sobrinus cosyltransferase U (GTF-U). Peptide fragments of GTF-U, especially
                                                                  Geel- Schutten
                                         2003-289780/28
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IPTYSFVRAHDSEVQTVIAKIV 578
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2002US-0402483P.
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                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                               TOEGEPAST
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Pred. No. 0.00
4; Mismatches
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RESULT 29
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Best Local S
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glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in mutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a semicorporate as a semicorporated in mutritions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterium on sucrose substrate, and having backbone consisting of alpha (1,3) - and alpha (1,6) -linked anhydroglucose units, useful as thickener.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 29; 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucan; glucosyltransferase activity; thickener; prebiotic; bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
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                                                                                                                                                                                                         Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener
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25-JUL-2001;
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                                                                                                                                                                                                                                                                                                                              Van Geel-
                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                              (NEDE ) NEDERLANDSE ORG
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DB; ACC50071.
                                                                                                                                                                              11; Page 25-26; 51pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 AA;
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2001EP-00202841.
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Pred. No. 3.7e-05;
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Best Local Similarity
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                                                                                                                                                     The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the glastrointestinal tract. The present sequence represents a sequence of the
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-289780/28.
N-PSDB; ACC84450.
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                                                                                                                                                                                                                                                                                                                                 Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3) - and alpha (1,6)-linked anhydroglucose units, useful as thickener.
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25-JUL-2001; 2001EP-00202841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Geel- Schutten GH;
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                                                                                                                  Sequence 1497 AA;
                                                                                                                                            glucansucrase gene
                                                                                                                                                                                                                                                                                                         Claim 11; Fig 1; 51pp; English.
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142 PNYTFIRAHDSEVQTIIAQII 162
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l5; Conservative
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                           PSYSFARAHDSEVQDIIRDII 22
                                                         Conservative
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Pred. No. 0.0012;
2; Mismatches 4; Indels
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Pred. No.
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Search completed: May

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VPSYSFARAHDSEVQDITRDII
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F;1222-1241/Domain: cpl 1
F;1287-1306/Domain: cpl 1
F;1380-1351/Domain: cpl 1
F;1390-1351/Domain: cpl 1
F;1352-1371/Domain: cpl 1
F;1462-1420/Domain: cpl 1
F;1462-1420/Domain: cpl 1
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A,Title: Peptide sequences for sucrose splitting and glucan binding within Streptococcus A,Reference number: A38175; MUID:91123227; PMID:1704006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1592 < ABO>
A;Description: catalyzes the synthesis of both water-soluble and water-insoluble (Symporfamily: cpl repeat homology C;Keywords: duplication; glycosyltransferase; hexosyltransferase F;1-34/Domain: signal sequence #status predicted <SIG-F;35-1375/Product: glucosytransferase #status predicted <WAT>F;1126-1145/Domain: cpl repeat homology <CP2>F;1123-1272/Domain: cpl repeat homology <CP2>F;11318-1337/Domain: cpl repeat homology <CP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 69, 101-109, 1988
A;Title: Sequence analysis of the gtfC gene from Streptococcus
A;Reference number: JT0345; MUID:89137980; PMID:2976010
A;Accession: JT0345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dextransucrase (EC 2.4.1.5) precursor - Streptococcus N;Alternate names: sucrose 6-glucosyltransferase
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R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
T. Bacteriol. 19470, 1987
J. Bacteriol. 19473
A;Title: Sequence analysis of the 9tfB gene from Streptococcus mutans.
A;Reference number: A33135; MUID:87308013; PMID:3040685
A;Accession: C33135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: JT0345; C33135
R;Ueda, S.; Shiroza, T.; Kuramitsu,
                                                                                                                                                                                                                     A;Gene: gtfC
                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-349 <SHI>
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A; Residues: 1-1375 < UED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Streptococcus mutans;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992
                                                                                                                                                                                                  ;Function:
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Pred. No. 6.6e-09;
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gtfB protein precursor - Strepto
C;Species: Streptococcus mutans
C;Date: 23-Oct-1990 #serror
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A;Residues: 1-14/5 <SHI>
A;Residues: 1-14/5 <SHI>
A;Cross-references: GB:M17361; NID:g153639;
R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: strain GS-5 C;Superfamily: cpl repeat homology C;Superfamily: cpl repeat homology F;1096-1115/Domain: cpl repeat homology F;1224-1243/Domain: cpl repeat homology F;1289-1308/Domain: cpl repeat homology F;1354-1373/Domain: cpl repeat homology F;1419-1438/Domain: cpl repeat homology
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A;Accession: B33135
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J. Bacteriol. 169, 4263-4270, 1987
A;Title: Sequence analysis of the gtfB gene
A;Reference number: A33135; MUID:87308013; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 C;Accession: B33135; A33128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A33128
A;Accession: A33128
A;Status: preliminary; not
                                                                                                                                                                                                                                                                                            Gene 182, 23-32, 1996
A; Title: Cloning and sequencing of a gene coding for a novel
A; Reference number: JC5473; MUID: 97136886; PMID: 8982063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-171, 173-641, 'N', 643-1475
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                                                                      C;Keywords: glycosyltransferase; hexosyltransferase F;78-870/Domain: catalytic #status predicted <CAT> F;922-1290/Domain: glucan-binding #status predicted
                                                                                                                                                                                              A;Residues: 1-1290 <MON>
A;Cross-references: GB:U38181
                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Leuconostoc mesenteroides
C;Date: 07-Jul_1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
                                                                                                                                    A;Gene: derA
                                                                                                                                                                            C; Comment: This
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86.4%;
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binding #status predicted
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Score 85; DB Pred. No. 4.9e
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Pred. No. 4.5e-07;
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Pred. No. 7
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R; Monchois, V.; Remaud-Simeon, M.; Monsan, P.; Willemot, PEMS Microbiol. Lett. 159, 307-315, 1998
A; Title: Cloning and sequencing of a gene coding for an A; Reference number: Z20981; MUID:98164374; PMID:9503626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable dextransucrase (BC 2.4.1.5), extracellular - Leuconostoc mesenteroides C;Species: Leuconostoc mesenteroides C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
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A;Residues: 1-1599 <JAC>
A;Residues: 1-1599 <JAC>
A;Residues: 1-1599 <JAC>
A;Cross-references: EMBL:Z11872; NID:g47530; PIDN:CAA77898.1; PID:g47531
A;Experimental source: ATCC 25975
A;Experimental source: ATCC 25975
A;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A.
J. Gen. Microbiol. 137, 2577-2593, 1991
A;Title: Molecular characterization of a cluster of at least two glucosy
A;Reference number: A44811; MUID:92148377; PMID:1838391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucosyltransferase (BC 2.4.1.-) S - Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_changC;Accession: S22737; S28810; B44811; S22727
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A;Cross-references: EMBL:AF030129; NID:g2766611; PID:g2766612;
A;Experimental source: strain NRRL B-1299
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Rijacques, N.

Bubmitted to the EMBL Data Library, March 1992
A;Reference number: S22726
A;Accession: S22737
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C;Keywords: glycosyltransferase; hexosyl
F;1456-1475/Domain: cpl repeat homology
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A; Residues: 1-51 <GIF>
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  TYLFVRAHDSEVQTVIADII 593
                                        SYSFARAHDSEVQDIIRDII 22
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70.0%;
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Pred. No.
                                                                                                       Score 72; DB 2;
Pred. No. 0.0073;
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glucosyltransferase - Streptococcus salivarius C;Species: Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C;Accession: T30857 R;Simpson, C.L.; Giffard, P.M.; Jacques, N.A.
                                                                                                                         Infect. Immun. 58, 2452-2458, 1990
A,Title: Analysis of the Streptococcus downei gtfS gene, A,Reference number: A41483, MUID:90316665; PMID:2142479
A,Ression: A41483
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T30552
Glucosyltransferase N - Streptococcus salivarius (fragment)
C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_ch
C;Accession: T30552
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A; Residues: 1-1449 <SIM>
A; Cross-references: EMBL
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                                                                                                                                                                                                                                 glucosyltransferase (EC 2.4.1.-) gtfS precursor - Streptococcus sobrinus C;Species: Streptococcus sobrinus C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999 C;Accession: A41483
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A;Residues: 1-1449 <JAF>
A;Cross-references: EMBL:AF049609; NID:g2935545; PID:g2935546; PIDN:AAC05156.1
C;Genetics:
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A;Description: Streptococcus salivarius V1477
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A;Gene: gtfS
C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                 A; Molecule type:
A; Residues: 1-13
                                                                             A;Cross-references: GB:M30943; NID:g153652; PIDN:AAA26898.1;
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mber: Z20854
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70.0%;
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Pred. No. 0.01
2; Mismatches
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Pred. No.
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RESULT 10
A44811
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C;Species: Streptococcus salivarius
C;Species: Streptococcus salivarius
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 15-Oct-1999
C;Accession: A44811; S2726; S28809
R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A.
J. Gen. Microbiol. 137, 2577-2593, 1991
A;Title: Molecular characterization of a cluster of at least two glucosyltransferase.
A;Reference number: A44811; MUID: 92148377; PMID:1838391
A;Accession: A44811
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A;Gene: gtfJ
C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; h
F;1307-1326/Domain: cpl repeat hom
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A;Residues: 1-1518 <GIF>
A;Residues: 1-1518 <GIF>
A;Cross-references: EMBL:Z11873; NID:g47526; PIDN:CAA77900.1; PID:g47527
A;Note: sequence extracted from NCBI backbone (NCBIN:81050, NCBIP:81052)
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A45866
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A;Residues: 1-1431 <HON>
A;Residues: GB:M29296
A;Cross-references: GB:M29296
C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexos
F;181-201/Domain: cpl repeat homology
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F;1192-1211/Domain: cpl repeat homology <CP3>
F;1257-1276/Domain: cpl repeat homology <CP4>
F;1277-1297/Domain: cpl repeat homology <CP5>
F;1321-1340/Domain: cpl repeat homology <CP8>
F;1341-1361/Domain: cpl repeat homology <CP6>
F;1341-1361/Domain: cpl repeat homology <CP6>
F;1385-1404/Domain: cpl repeat homology <CP7>
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13; Conserv
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   NYIFIRAHDSEVOTVIAKII 595
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                                     SYSFARAHDSEVODIIRDII 22
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68.2%;
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                                                                                          58.2%;
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Pred. No. 0.043;
3; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                      hexosyltransferase
                                                                          Score 64; DB pred. No. 0.12 2; Mismatches
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hypothetical protein sll1219 - Synechocystis sp. (strain PCC 6803)
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: PCC 6803
A; Variety: PCC 6803
C; Accession: S75540
C; Accession: S75540
C; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Pco, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada DNA Res. 3, 109-115, 1396
DNA Res. 3, 109-136, 1396
DNA Res. 3, 109-136, 1396
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosyltransferase - Streptococcus salivarius
C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30858
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S75540
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A; Residues: 1-1577 <SIM>
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                                                                                                                                                             galactose-1-phosphate uridyltransferase galT [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 27-Oct-2003
C;Accession: E83788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18101.1; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June C;Superfamily: Synechocystis hypothetical protein s111219
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A; Residues: 1-108 < KAN>
                                                    A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: E83788
                                                                                                                 C;Accession: E83788
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.;
Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                 В
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A;Residues:
                   A; Molecule type:
                                       A;Status: preliminary
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3, 609-621, 1995
                     DNA
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Pred. No. 0.13
4; Mismatches
                                                                                                                                                                                                                                                                                                                                     51
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                                                                                                        Bacillus halodurans
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Yamada, M.; Yasud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PID:g165318
; 1996
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and Hira

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A;Cross-references: EMBL:X52282; NID:g28705; PIDN:CAA36523.1; PID:g28706
A;Note: alternative splice form C6
R;Porter, J.G.; Arfsten, A.; Fuller, F.; Miller, J.A.; Gregory, L.C.; Lewicki, J.A.
Blochem. Biophys. Res. Commun. 171, 796-803, 1990
A;Title: Isolation and functional expression of the human atrial natriuretic peptide cle
A;Reference number: A35896; MUID:90386656; PMID:2169733
A;Accession: A35896
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A;Experimental source: strain C-125
R;Stults, J.T.; O'Connell, K.I.; Garcia, C.; Wong, S.; Engel, A.M.; Garbers, D.L.; Biochemistry 33, 11372-11381, 1994
A;Title: The disulfide linkages and glycosylation sites of the human natriuretic pe A;Reference number: A55870; MUID:95244450; PMID:7727388
A;Contents: annotation; propeptide, disulfide bonds, carbohydrate binding sites
                                                                                                           A;Molecule type: mRNA
A;Residues: 1-475,'SG',477-540 <POR>
A;Cross-references: GB:M59305; NID:g178651; PIDN:AAA51734.1; PID:g178652
A;Note: alternative splice form C5
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A; Accession: T47184
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submitted to the Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lowe, D.G.; Camerato, T.R.; Goeddel, D.V.

Ricleic Acids Res. 18, 3412, 1990

A;Title: CDNA sequence of the human atrial natriuretic peptide clearance receptor.

A;Reference number: S10150; MUID:90287735; PMID:2162522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 05-May-1995 #text_change 22-Jun-1999
C;Accession: S10150; A35896
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A; Residues: 1-506 < AAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: atrial
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A;Experimental source: adult testis;
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3412, 1990
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Pred. No.
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Pred. No. 8.9;
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                                                     peptide
                                                                                                    Lowe
           glutamyl-tRNA synthetase [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Pate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: A89820 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi. I.:
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                                                                                                                                                   RESULT 18
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C;Keywords: alternative splicing; glycoprotein; homodimer; hormone receptor; transplicing; glycoprotein; homodimer; hormone receptor; transplicing; glycoprotein; homodimer; hormone receptor; ransplicing; glycoprotein; homodimer; hormone receptor; rid-45/Domain: signal sequence #status predicted <SIG>
F;24-45/Domain: propeptide #status experimental cPRO>
F;46-540/Product: natriuretic peptide receptor C #status predicted <MAT>
F;46-479/Domain: extracellular #status predicted <EXT>
F;131-462/Domain: natriuretic peptide-binding domain homology <NPB>
F;483-503/Domain: transmembrane #status predicted <TMM>
F;483-503/Domain: transmembrane #status predicted <TMM>
F;486,293/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;108-136,213-261/Disulfide bonds: #status experimental
F;394/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F;394/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: bacC
C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;505-946/Domain: acetate-CoA ligase homology <ACL1>
F;564-1032/Domain: acyl carrier protein homology <ACL2>
F;1542-1976/Domain: acyl carrier protein homology <ACL2>
F;1946-2063/Domain: acyl carrier protein homology <ACL2>
F;1996-2063/Domain: acyl carrier protein homology <ACL3>
F;1046-3483/Domain: acyl carrier protein homology <ACL3>
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A;Map position: 5p14-5p13
C;Superfamily: natriuretic peptide receptor C; natriuretic
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A;Title: The bacitracin biosynthesis operon of Bacillus 1
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C;Genetics:
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                                                                                                                                                                                                                            F;4542-4609/Domain: acyl carrier protein homology <ACP4>
F;5593-6032/Domain: acetate-CoA ligase homology <ACL5>
F;6050-6118/Domain: acyl carrier protein homology <ACP5>
F;3532/Binding site: phosphopantetheine (Ser) (covalent)
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F;4078-4526/Domain: acetate-CoA ligase homology <P
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A;Residues: 1-6359 <KON>
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Pred. No. 4.9e+02;
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iroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.;
A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano,

Yuzawa, H.; Kobayashi, T.; Inoue, R.; Kaito,

R.; Kaito, C.;

; Cui, L.; Sekimizu,

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RESULT 19
G82455
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89820
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C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
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Nature 406, 477-483, 2000
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A;Experimental source: strain N315
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A; Residues: 1-51 <HEI>
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                                                                                                                                      R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: A;Reference number: A82870 A;Recession: F82935
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                                                 ;Cross-references: GB:AE002108; (;Experimental source: serovar 3;
                                                                                     ;Status: preliminary
;Molecule type: DNA
;Residues: 1-597 <GLA>
                                                                                                                                                                                                                              ;Date: 18-Aug-2000 #sequence_revision;Accession: F82935
                                                                                                                                                                                                                                                                    ;Species: Ureaplasma urealyticum
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dnaX; UU087
ic code: SGC3
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                                                      GB:AF222894; NID:g6899034; PIDN:AAF30492.1; blovar 1
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Pred. No. 2
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H.; Dragoi,
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I.; Sellers,
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C;Keywords:
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Best Local :
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: H90599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: H95599
                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamate-tRNA ligase (EC 6.1.1.17) [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002 C;Accession: F98106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: MYPU 7040
A;Genetic code: SGC3
C;Superfamily: conserved hypothetical protein
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A; Residues: 1-631 < KUR>
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                                                                                                                                                                                                                                                                                                                                                            R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, & e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                        A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-486 < KUR>
                                                                                                                                                                                                                A;Cross-references: GB:AE007317;
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Best Local S
Matches 8
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                                                                                                                                                          ;Gene: gltX
;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
                                                                                     Query Match
Best Local :
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es 5; Conserv
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8; Conserv
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                              PSYSFARA---HDSEVQDIIR 19
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nilarity 29.4%;
Conservative
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Pred. No.
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Pred. No.
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                                                                                       Score 44.5;
Pred. No. 4
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46;
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Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; ok, C.; Schlueter, Boland, J.A.; a, Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, R;Glaser, P.; Frangeul, G.; Duchaud, E.; Durand, L.; J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; J.
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                                   C;Species: myxoma virus
C;Date: 13-Jan-1995 #sequence_revision
C;Accession: §31626
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                                                                                                                                                                                                                                                                                                                                                   A;Gene: uvrc
C;Superfamily: excinuclease ABC chain
                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-603 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96428.1; PID:g16413656; GSPDB:GN00178
A:Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, B.; Maitournam, A.; M. ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AD1582
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C; Superfamily:
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A; Residues: 1-603 < GLA>
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
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                                                                                                                                         RESULT 25
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Matches
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Library, January 1993
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Pred. No. 56;
7; Mismatches
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Pred. No. 56
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                                                             13-Jan-1995
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Dussurget, O.; Entian, K.D.;
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Fsihi, H.
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Fsihi, H.
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Glodek, A., Zhou, L., Overbeek, R.; Gocayne, J.D.; Weidman, G.G.; Gill, S.; Kirkness, E Nature 390, 364-370, 1997

A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.

A,Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa A;Reference number: A69250; MUID:98049343; PMID:9389475

A,Racession: F69471
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A;Reference number: S31626
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 < JAC>
A;Residues: 1-188 < JAC>
A;Cross = references: EMBL:Z19600; NID:g60609; PIDN:CAA79660.1; PID:g60610
C;Superfamily: vaccinia virus 14K cell fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AF1336
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
R;Glaser, P.; Frangeul, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; i
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                                                                                                                                                                                                                                                                                                                                                                                                    atrazine chlorohydrolase homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                             R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 294, 849-852, 2001
                                                                                        A;Cross-references: GB:AE000980;
                                                                                                           A; Residues: 1-330 < KLE>
                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
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Best Local :
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Local Similarity 35.3%;
les 6; Conservative
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                     Local
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Similarity
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                                                                                   GB:AE000782; NID:g2689303; PIDN:AAB89475.1; PID:g264877
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44;
Pred. No.
                       Score 44; DB
Pred. No. 34;
                                                                                                                                                         sequence not shown; translation
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21;
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Mismatches

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N,Alternate names: reverse transcriptase
C;Species: Drosophila melanogaster
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 16-Jun-2000
C;Accession: A03971
R;Saigo, K.; Kugimiya, W.; Matsuo, Y.; Inouye, S.; Yoshioka, K.; Yuki, S.
Nature 312, 659-661, 1984
A;Title: Identification of the coding sequence for a reverse transcriptase-like enzyme
A;Reference number: A93349; MUID:85061628; PMID:6209583
A;Accession: A03971
A;Molecule type: DMA
A;Residues: 1-1058 <SAI>
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A;Cross-references: FlyBase:PBs
C;Superfamily: pol polyprotein
C;Keywords: polyprotein; rever
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                                                               RESULT 30
F83819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C. Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein lmo0146 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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C;Genetics:
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hypothetical protein BH1358 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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Best Local Similarity 40.0%;
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152 AYSSARDHDLKLMEEVREI 170
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Pred. No. 1.3e+02
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: F83819
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                                                                                                                                                                                          A;Molecule type: DNA A;Rosidues: 1-176 <STO> A;Rosidues: 1-176 <STO> A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05077.1; GSPDB:GN0(A;Experimental source: strain C-125
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                                                                                                                                                       A;Gene: BH1358
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P13470
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  cyanidium
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8 anabaena sp

6 synechocyst

5 wiggleswort

5 methanococc

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2 aeropyrum p

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Best Local !
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P27470;
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRDO
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGH
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DEWTAL PLAQUE BEC-
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
-!- CATALYTIC ACTIVITY: Sucrose + {(1,6)-11pha-D-glucosyl) (N) = D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FACTOR (SERVICE G)
STRAIN=6715 / Serotype G;
MEDLINE=91133227; PubMed=1704006;
MEDLINE=91133227, FubMed=1704006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5)
(Sucrose 6-glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus sobrinus synthetase).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES BOTH WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus downei (Streptococcus sobrinus)
                                                                                                           REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            EMBL; D90213; BAA14241.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Péptide sequences for sucrose splitting and glucan binding within
Streptococcus sobrinus glucosyltransferase (water-insoluble glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                               InterPro; I
                                                                                                                                      REPEAT
                                                                                                                                                                  REPEAT
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                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                       Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 173:989-996(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to family 70 of glycosyl hydrolases.
SIMILARITY: Contains 16 cell wall binding repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fructose + {(1,6)-alpha-D-glucosyl}(N+1).
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORMS OF GLUCANS
 548
                                                                                                                                                                                                                                                                                                      Pro; IPR002479; CW_binding.
Pro; IPR003318; Glyco hydro_70.
PF01473; CW_binding_1; 13.
PF02324; Glyco_hydro_70; 1.
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                                                                    Similarity
                  VPSYSFARAHDSEVQDIIRDII
 VPSYSFARAHDSEVQDIIRDII 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T., Kodama
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                                                                                                                                                                                                                                                                                         transferase; Signal; Repeat; Dental caries.
                                                                                                            176167
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                                                                                                                           70.04
                                                                                                                                                                                                                      GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
6.5 X TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                    Score 110; DB 1;
Pred. No. 4.6e-09;
                                                                                                                           (INCOMPLETE)
                             22
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohta H.,
                                                                                                               BC0A66D079351ECF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GTF-I)
                                                                                  Length 1592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Dextransucrase)
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01-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTF1
                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGH TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECOF THEIR ABILITY TO ADEERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
-!- CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = D-fructose + {(1,6)-alpha-D-glucosyl}(N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glucosyltransferase-I precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus.
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-!- SIMILARITY: Belongs to family 70 of glycosyl hydrolases.
-!- SIMILARITY: Contains 19 cell wall binding repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence of a glucosyltransferase sobrinus MFe28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87308014; PubMed=3040686;
Ferretti J.J., Gilpin M.L., Russell R.R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                          DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                      InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                      EMBL; M17391; AAC63063.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 169:4271-4278(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                             SEQUENCE
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1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZE
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 \vdash
                                       Similarity
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VPSYSFARAHDSEVQDIIRDII
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                            Conservative
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Lactobacillales; Strepto
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95.5%;
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A REPEAT.
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GLUCOSYLTRANSFERASE-I.

CATALYTIC (APPROXIMATE).

CATALYTIC (APPROXIMATE).
                           Score 108; DB 1;
Pred. No. 9.6e-09;
1; Mismatches 0
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                                                      Length 1597;
                                                                                 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Dextransucrase)
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VPSYSFARAHDSEVODLIRDII 575

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RESULT 3
GTFB_STRMU
ID GTFB_S
  P08987; O69381; O69384;
01-NOV-1988 (Rel. 09, C
28-FEB-2003 (Rel. 41, I
10-OCT-2003 (Rel. 42, I
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Shiroza T., Ueda S., Kuramitsu H.K.;
"Sequence analysis of the gtfB gene from
J. Bacteriol. 169.4263-4270(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Sucrose 6-glucosyltransferase). GTFB OR SMU.1004.
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Proc. Natl.
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                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in oway ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.lsb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     MISCELLANBOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE (
1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S (
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI
FORMS OF GLUCANS.
SIMILARITY: Belongs to family 70 of glycosyl hydro
SIMILARITY: Contains 10 cell wall binding repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

FUNCTION: PRODUCTION OF EXTRACELULIAR GLUCANS, THAT ARE THE THOUSE IN THE EDVELOPMENT OF THE DENTAL PLAQUE OF THEIR ABILLITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE I AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS. CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = fructose + {(1,6)-alpha-D-glucosyl}(N+1).

SUBCELLULAR LOCATION: Secreted.
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                    M17361; AA; D88651; BA; D88654; BA; D88657; BA; D88660; BA; D89977; BA; AE014940;
  взз135;
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                                       ; AAA88588.1; -...; BAA26101.1; -...; BAA26105.1; -...; BAA26109.1; -...; BAA26119.1; -...; BAA26119.1; -...
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precursor (EC 2.4.1.5)
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O69387; O69390; O69396;
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InterPro; IPR003318; Glyco hydro_70.
Pfam; PF0473; CW_binding_1; 7.
Pfam; PF02324; Glyco_hydro_70; 1.
Transferase; Glycosyltransferase; Signal; Repeat;
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S -> F
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GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE)
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                     Score 103;
Pred. No. 5
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                 Gaps
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RESULT 4
GTFC_STRMU
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"Sequence analysis of the gtfB gene from Streptococcus mutans.";

I. Bacteriol. 169:4263-4270 (1987).

C. I. Bacteriol. 169:4263-4270 (1987).

C. I. PUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

I. CATALYTIC ACTIVITY: Sucrose + {(1,6)-4]pha-D-glucosyl}(N) = D-fructose + {(1,6)-4]pha-D-glucosyl}(N+1).

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. SILNKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA FORMS OF GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF GLUCANS (ALPHA 1,6-GLUCOSE).
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01-NOV-1988 (Rel
28-FEB-2003 (Rel
10-OCT-2003 (Rel
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SECUTION OF THE STRAIN-MT4239 / Serotype C, MT4245 / Serotype C;
MT4467 / Serotype E, and MT8148 / Serotype C;
MEDLINE=98231643; PubMed=9570124;
Fujiwara T., Terio Y., Hoshino T., Kawabata S
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-SI precursor (EC 2.4.1.5) (C
Dextransucrase) (Sucrose 6-glucosyltransferase)
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MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D., McShan W.M., McLaughlin R.E., Jia H., Lin S.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
"Genome sequence of Streptococcus mutans UA159, a cariogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
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Sequence analysis of the gtfC
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SIMILARITY: Contains
                                                                                                    European
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                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration -
 M22054;
D88652;
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                                           the Swiss Institute of Bioinformatics pean Bioinformatics Institute. There non-profit institutions as long as and this statement is not removed. Urequires a license agreement (See htt an email to license@isb-sib.ch).
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BAA26102.
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EMBL; D88661; BAA26110.1; -.
EMBL; D89661; BAA26120.1; -.
EMBL; D89978; BAA26120.1; -.
EMBL; M17361; AAA88589.1; -.
EMBL; M17345, J70345, CW binding.
InterPro; IPR002479; CW binding.
InterPro; IPR00318; Glyco hydro 70.
Pfam; PF01473; CW binding 1; 8.
Pfam; PF01274; Glyco hydro 70; 1.
Transferase; Glycosyltransferase; Sign
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DGH -> NGY (IN STRAIN GS-5, MT4467 AND MT8148).

MISSING (IN STRAIN MT4245).

I -> V (IN STRAIN MT8148).

T -> A (IN STRAIN MT8148).

T -> A (IN STRAIN MT8148).

R -> K (IN STRAIN MT8148).

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GRLYFKSNGTVQAKGELITERKGRIKYYDDENGUEVRNYVR GRLYFKSNGTVQAKGELITERKGRIKYYDDENGUVRYXASHD QRNHWDYDYRRDFGRGSSSAVRFRHSRNGFFDNFFRF -> HASILSLMVFRLESSLQSVKVVSNTMILLPEMKFVIVM
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GLUCAN-BINDING (APPROXIMATE).
2.4 A, 1 C AND 1 AC REPEATS.
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InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW binding 1; 8.
Pfam; PF02324; Glyco_hydro_70; 1.
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                                       167296B5A2E8C476
                                                                                                                   Signal; Repeat; Dental caries
                     No.
                                                                                                               (POTENTIAL)
                                           C (APPROXIMATE).
BINDING 3.
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BINDING 2.
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                 6,
                           Length 1365;
                                       CRC64;
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Gilmore K.S., Russell R.R., Ferretti J.J.;

Gilmore K.S., Russell R.R., Ferretti J.J.;

glicosyltransferase that synthesizes soluble glucans.*;

glicosyltransferase that synthesizes soluble glucans.*;

Infect Immun. 58:2452-2458(1990).

-!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT

TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-!- CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = D-

fructose + {(1,6)-alpha-D-glucosyl}(N+1).

-!- ENZYME REGULANION: GITE-S SYNTHESIS BY GTF-S IS INDEPENDENT OF
PRIMER GLUCAN UNLIKE GTF-I.

-!- MISCELLANSOUS: GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA

-!- MISCELLANSOUS: GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA).
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P29336;
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10-OCT-2003
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SIMILARITY: Belongs to family 70 of glycosyl hydrolases. SIMILARITY: Contains 10 cell wall binding repeats.
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                                                               , 6-GLUCOSE)
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(Rel. 24,
(Rel. 42,
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; Lactobacillales; Streptococcaceae;
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RESULT 6
GTFD_STRMU
 GIFD STRMU STANDARD; PRT; 1462 AA. PA9331; 069383; 069386; 069389; 069392; 0693 01-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Glucosyltransferase-S precursor (EC 2.4.1.5 (Sucrose 6-glucosyltransferase).
EMBL; M29296; J
EMBL; D88653; E
EMBL; D88656; E
EMBL; D88659; E
EMBL; D88662; E
EMBL; D89779; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MT4239 / Serotype C, MT4245 / Serotype MT4467 / Serotype E, and MT8148 / Serotype C;
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Carson M.B., Primeaux C., Tian R., Kenton S., J
Li S., Zhu H., Najar F., Lai H., White J., Roe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutans.";
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                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22295063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=UA159 / ATCC 700610 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMS Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular analyses of glucosyltransferase
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                                                                                                       or send an
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                                                                                                                                                                                                                                                                        fructose + {(1,6)-alpha-D-glucosyl}(N+1).
SUBCELLAULAR LOCATION: Secreted.
MISCELLAUBOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALIMISCELLANBOUS: GTF-I SYNTHESIZES WATER-INKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-SI SYNTHESIZES 1,3-LINKED GLUCOSE AND SOME 1,6-GLUCOSE). GTF-SI SYNTHESIZES
                                                                                                                                                                                                                                                                                                                                                C. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAL OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CRIALYTIC ACTIVITY: Sucrose + { (1,6) -alpha-D-glucosyl} (N) = D-GRIALYTIC ACTIVITY: Sucrose + { (1,6) -alpha-D-glucosyl} (N)
                                                                                                                                                                                                                            SIMILARITY: Belongs to family 70 of glycosyl hydrolases SIMILARITY: Contains 6 cell wall binding repeats.
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FORMS OF GLUCANS.
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                                                                                                        equires a license agreement (Semail to license@isb-sib.ch).
 ; AAA26895.1; -.; BAA26103.1; -.; BAA26107.1; -.; BAA26111.1; -.; BAA26115.1; -.; BAA26121.1; -.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=12397186;
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InterPro; IPR002479; CW_binding.
InterPro; IPR00231B; Glyco hydro_70.
Pfam; PF01473; CW_binding_1; 11.
Pfam; PF02324; Glyco hydro_70; 1.
Transferase; Glycosyltransferase; Signal; Repeat; Dental caries;
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                 SYSFARAHDSEVQDIIRDII
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D -> Y (IN STRAIN MT4251).

E -> K (IN STRAIN MT4245 AND MT4251).

I.G -> IR (IN STRAIN MT4245).

G -> R (IN STRAIN MT4245).

G -> R (IN STRAIN MT4245).

G -> R (IN STRAIN MT4239).

H -> Q (IN STRAIN MT4239).

Y -> C (IN STRAIN MT4239).

Y -> C (IN STRAIN MT4251 AND MT4467).

F -> L (IN STRAIN MT4251).

O -> P (IN STRAIN MT4245).

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R -> K (IN STRAIN MT42467).

G -> R (IN STRAIN MT42467).

R -> R (IN STRAIN MT4467).

R -> R (IN STRAIN MT4467).

R YYDKNGCMMYYNKVYTLAMGRRIGIDRWGJARYY -> V.

R (IN REF. 1).
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D -> N (IN STRAINS MT4239, MT4245 AND MT4251).

MT4251).

Q -> H (IN STRAIN MT4245).

D -> N (IN STRAIN MT4239) AND MT4251).

E -> K (IN STRAIN MT4239).

V -> F (IN STRAIN MT4239).

F -> L (IN STRAIN MT4239).
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TDQGSEA -> :

TDQGS -> AD

MT4245).

T -> A (IN
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                                    Score 64; DB 1;
Pred. No. 0.069;
2; Mismatches
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V (IN STRAIN MT4245).
T (IN STRAIN MT425)
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AC QPROT2; QPRC74;
DT 16-CCT-2001 (Rel. 4
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A Takami H., Takaki Y., Nakasone K., Sakiyama T., Maeno G., Sasaki A Hirama C., Fuji F., Masui N.;
A Hirama C., Fuji F., Masui N.;
T "Genetic analysis of the chromosome of alkaliphilic Bacillus that the chromosome of alkaliphilic Bacillus 1:27-233 (1999).
Extremophiles 3:227-233 (1999).
C --- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose 1-phosphate + UDP-galactose.
C --- PATHWAY: Galactose metabolism; second step.
C --- SUMCELLULAR LOCATION: Cytoplasmic (Potential).
C --- SIMILARITY: Belongs to the galactose-1-phosphate uridylyltransferase family 2.
                                                                                                                                                                                                                         HAMAP, MF 00571; -; 1.

HAMAP, MF 00571; -; 1.

InterPro; IPR000766; GalP_Utransf_C.

InterPro; IPR005850; GalP_Utransf_N.

InterPro; IPR005849; GalP_Utransf_N.

InterPro; IPR005934; GalP_Utransf_N.

Pfam; PF01744; GalP_UDP_transf; 1.

Pfam; PF01087; GalP_UDP_transf; 1.

TIGRPAMs; TIGR01239; galT_2; 1.

PROSITE; PS01163; GALP_UDP_TRANSF_II; 1.

PROSITE; PS01163; GALP_UDP_TRANSF_II; 1.

Complete proteome.

SEQUENCE 508 AA; 57989 MM; 16AP6F6607F
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SEQUENCE FROM N.A.
SERAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.1:
uridylyltransferase) (UDP-glucose--hexose-1-phosphate
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EMBL; AB024554; BAA83925.1; -.
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1; Mismatches
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., Kuhara S
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HAMAR; MF 00022; -; 1.
InterPro; IPR004527; GltX bact.
InterPro; IPR00924; Glu TRNA-synt lc.
InterPro; IPR008925; tRNA-synt bind.
InterPro; IPR008925; tRNA-synt I.
InterPro; IPR001412; tRNA-synt I.
Pfam; PF00749; tRNA-synt lc; 1.
PRINTS; PR00987; TRNASYNTHGLU.
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Q8CTU3;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis strain (ATCC 12228).";
Mol. Microbiol. 49:1577-1593(2003).
-i- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP
                                                                                                                                                                               HUMAN
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  28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Atrial natriuretic peptide clearance receptor precursor (ANP-C)
(ANPRC) (NPR-C) (Atrial natriuretic peptide C-type receptor).
                                                                                                    P17342;
01-AUG-1990
                                                                                                                                                       ANPC HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y.-Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12950922;
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Bacteria; Firmicutes; Bacil
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SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
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Last annotation updat
ase (EC 6.1.1.17) (Glu
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Pred. No. 1:
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                            GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR0011928; ANF receptor.
InterPro; IPR001170; Ntpep_receptorN.
Pfam; PF01094; ANF receptor; 1.
PRINTS; PR00255; NATPEPTIDER.
PROSITE; PS00458; ANF_RECEPTORS; 1.
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and functional expression of the human atrial natriuretic peptide clearance receptor cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=90386656; PubMed=2169733;
POITE J.G., Arfsten A., Fuller F., Miller J.A., Gregory L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90287735; PubMed=2162522; Lowe D.G., Camerato T.R., Goeddel
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                                CHAIN
                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http:\bar{//www}.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBUNIT: Homodimer; disulfide-linked.
-i- SUBCELLULAR LOCATION: Type I membrane protein
-i- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 18:3412-3412(1990)
                                                                                                                                                                                                                                                         EMBL; AF025998; AAB88801.1;
PIR; S10150; OYHUCR.
                                                                                                                                                                                                                                                                                           EMBL; X52282; CAA36523.1; -. EMBL; M59305; AAA51734.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.";
Submitted (NOV-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rae J.L., Shepard A.R.;
"Human lens epithelial mRNA for atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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DOMAIN
                                                  SIGNAL
                                                                                                                                                                                                            MIM; 108962;
                                                                                                                                                                                                                           Genew; HGNC:7945; NPR3.
                                                                                                                                                                                                                                          PDB; 1JDN; 05-SEP-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cDNA sequence of the human atrial natriuretic
                                                                3D-structure.
                                                                               Receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOId=P17342-2; Sequence=VSP_001812;
MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS:
MITH GUANYLATE CYCLASE ACTIVITY (AND-A AND AND-B) AND ONE (ANP
WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM TH
CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SINILARITY: TO AND-A AND AND-B RECEPTORS IN THEIR EXTRACELLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND TRANSMEMBRANE DOMAINS.
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                                541
   481
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                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Commun. 171:796-803(1990)
                                                                               Transmembrane; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
   EXTRACELLULAR (POTENTIAL)
                                   ATRIAL NATRIURETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.V.;
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                                     CLEARANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clearance
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Best Local S
Matches 8
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bacitracin synthetase 3 (BA3) [Includes: ATP-dependent isoleucine
adenylase (IleA) (Isoleucine activase); ATP-dependent D-phenylalanine
adenylase (D-Phenyl (D-phenylalanine); ATP-dependent histidine
adenylase (HisA) (Histidine activase); ATP-dependent D-aspartate
adenylase (D-RapA) (D-aspartate activase); ATP-dependent asparagine
adenylase (D-RapA) (D-aspartate activase); ATP-dependent asparagine
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenylase (AsnA) (Asparagine activase); Aspartate racem (EC 5.1.1.13); Phenylalanine racemase [ATP hydrolyzing] (EC 5.1.1.11)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     068008;
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                                                                                                                                                                                                                                                                                                              -!- FUNCTION: INDUCES PEPTIDE SYNTHESIS, ACTIVATES AND INCORPORATES
FIVE ANINO ACIDS, FORMS A THIAZOLINE RING BETWEEN THE FIRST TWO
AMINO ACIDS AND INCOPORATES A D-GLUTAMINE IN THE FOURTH POSITION
-!- CATALYTIC ACTIVITY: L-aspartate = D-aspartate
-!- CATALYTIC ACTIVITY: ATP + L-phenylalanine = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                             Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus licheniformis.
Bacteria; Firmicutes; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                            Konz D., Klens A., Schoergendorfer K., Marahiel M.A.; "The bacitracin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecular characterization of three multi-modular peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=ATCC 10716;
                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                  synthetases.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98089193; PubMed=9427658;
N METHYLATION (OPTIONAL).

NISCELLANBOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC MISCELLANBOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC DODECAPERTIDES, THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST ABUNDANT IS BACITRACIN A, A BRANCHED CYCLIC DODECAPERTIDE. IT CONTINUES AN MITTHALL LINEAR PENTAPERTIDE MOIETY (ILLE-CYS-LEU-D-GLU-ILE) WITH AN ISOLEUCINE-CYSTEINE THIAZOLINE CONDENSATION PRODUCT AND A C-TERMINAL HEPTAPERTIDE RING (LYS-D-ORN-ILE-D-PHE-HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE C-
                                                                                                                            PATHWAY: Cyclic peptide antibiotic bacitracin biosynthesis.
SUBUNIT: LARGE MULTIENZYME COMPLEX OF BA1, BA2 AND BA3.

DOMAIN: CONSISTS OF FIVE MODULES WITH TWO EPIMERIZATION DOWAINS IN THE SECOND AND FOURTH MODULES, AND A PUTATIVE C-TERMINAL THIOESTERASE DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSITIATE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND
                                                                                                                                                                                                                                                                               phenylalanine.
COFACTOR: Contains 5
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                                                                                                                                                                                                                                                             (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                 Biol. 4:927-937(1997).
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
SG -> C (in isoform 2).
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BY SIMILARITY
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CYTOPLASMIC
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8A66415F7F7D62B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6359
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Best Local &
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Q99W75;
28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                              BINDING
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                           DOMAIN
BINDING
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REPEAT
REPEAT
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REPEAT
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pfam; pr00668; Condensation; 7.
pfam; pr00550; pp-binding; 5.
pfam; pr00975; Thioesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as modified and this statement is not removed. Use this requires a license agreement (See htters.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00012; PHOSPHOPANTETHEINE; 4.
PROSITE; PS00455; AMP_BINDING; 5.
PROSITE; PS50075; ACP_DOMAIN; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR006163; Pp_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
Staphylococcus aureus
Staphylococcus aureus
Staphylococcus aureus
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0154; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006162; Ppantne S. InterPro; IPR001031; Thioesterase.
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                             GLTX OR SAV0528 OR SA0486 OR MW0483.
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligase;
                                                                   Glutamyl-tRNA
                                                        (GluRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE. CONTAINS FOUR AMINO ACIDS IN THE D-CONFIGURATION (GLU-4, ORUPHE-9, AND ASP-11).
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 5 acyl carrier domains.
                                                                                                                                                                                        3186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P14687; 1AMU
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                                                                                                                                                                                                             1 VPSYSFARAHDSEVQDIIRDII
                                                                                                                                                                                                                                     ; TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isomerase;
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                                                                                                                                                                                                                                                                                              461
2999
4047
5549
966
1966
1983
3502
4544
6052
6082
                                                                   (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
(Rel. 41, Last annotation)
(Glu
                                                                                                                                                                                                                                     Conservative
                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                       2064
3570
4612
6129
1033
2064
3569
4610
6119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Antibiotic biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multifunctional
                                                                                                                                                                                                                                                 41.8%;
    y (strain Mu50 /
; (strain N315),
(strain MW2).
                                                                                                                                                                                                                                                                                   722923
                                                                                                                                                                                                                                    Score 46; DB
Pred. No. 2.3e
3; Mismatches
                                                                                                                                                                                                                                                                                   MW ;
                                                                                                                                                                                                                                                                                   PHOSPHOPANTETHEINE (B)
PHOSPHOPANTETHEINE (B)
PHOSPHOPANTETHEINE (B)
PHOSPHOPANTETHEINE (B)
PHOSPHOPANTETHEINE (B)
                                                                                                                                                                                                                                                                                                                                                      DOMAIN 5 (ASPARAGINE-AC
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 4.
ACYL CARRIER (ACP) 5.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                               al enzyme; Repeat.
IN 1 (ISOLEUCINE-ACTIVATING).
IN 2 (D-PHENYLALANINE-ACTIVATING).
IN 3 (HISTIDINE-ACTIVATING).
IN 4 (D-ASPARTIC ACID-ACTIVATING).
IN 5 (ASPARAGINE-ACTIVATING).
                                   ATCC 700699)
                                                                                                                                484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                      update)
) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                   .3e+02;
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E (BY SIMILARITY).
E (BY SIMILARITY).
E (BY SIMILARITY).
E (BY SIMILARITY).
                                                                                                                                                                                                                                                              Length 6359;
                                                                                                                                                                                                                                         Indels
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Staphylococcue

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RESULT 12
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Best Local Similarity
Matches 9; Conser
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InterPro; IPR004527; Glu tRNA-synt 1c.
InterPro; IPR009924; Glu tRNA-synt bind.
InterPro; IPR008925; tRNA-synt bind.
InterPro; IPR001412; tRNA-synt 1.
Pfam; PF00749; tRNA-synt 1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MUSO / ATCC 700699, and N315;
STRAIN-MUSO / ATCC 700699, and N315;
KUITCH AND COLOR OF THE MEDILINE-21311952; PubMed=11418146;
KUITCH AND COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF THE MEDILINE-COLOR OF 
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[2]
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SITE
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EMBL; AP004823; BAB94348.1;
PIR; A89820; A89820
HSSP; P27000; IGLN.
SWISS-2DPAGE; Q99W75; STAAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baba T., Takeuchi F., Kuroda M., Yu:
Nagai Y., Iwama N., Asano K., Naimi
Yamamoto K., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aureus
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[1]
  SYE_STRR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP003359; BAB56690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acquired MRSA."
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                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs; TIGR00464; gltX_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357:1225-1240(2001).
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| IPTYNFAVAIDDHYMQISDVIR 214
                                                                                                                                                             VPSYSFARA---HDSEVQDIIR 19
                                                                                                                                                                                                                                                                                                                                                                                               proteome.
                                                                                                                                                                                                                                                                                                   252
255
484 AA;
                                                                                                                                                                                                              Conservative
    STANDARD;
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256
255
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                                                                                                                                                                                                                                 41.48;
                                                                                                                                                                                                                                                                                                          ¥.
                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                           "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                 Score 45.5;
Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                              "HIGH" REGION
       PRT;
                                                                                                                                                                                                                                                                                                          4CBA5FF08DA23EFA
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yuzawa H., Aoki K.-I., Og
mi T., Kuroda H., Cui L.,
       486
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UVRC LISIN
ID "UVRC LISIN
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DT 10-0CT-2003
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Best Local S
Matches 9
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InterPro; IPR004527; GltX_bact.
InterPro; IPR000924; Glu_tRNA-synt_1.
InterPro; IPR008925; tRNA-synt_bind.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_1c; 1.
PRINTS; PR00987; TRNA-SYNTHGLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8CWN5;
10-OCT-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-21429245; PubMed=11544234;
Hoskins J., Alborn W.B. Jr., Arnold J., Blaszczak L.C., Burgett Hoskins J., Alborn W.B. Jr., Arnold J., Fu D.-J., Fuller W., Gering DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Gering Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeastex B.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeastex Mundy C.T., Rockey P., Sun P.-M., Winkler M.B., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatruc Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatruc
                                                                                                                                                                                                                                                                                                                  Complete
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + trnA(Glu) = AMP +
-!- CATALYTIC ACTIVITY: Similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-trnA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoni Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glass J.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=171101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLTX OR SPR1881.
                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0464; gltX_bact; 1.

PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

Aminoacyl-tRNA synthetase; ProteIn biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE008552; AAL00683.1; -. PIR; F98106; F98106.
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                            196
                                                                                                                                                                        N
                                                                                                                                                                                                       9;
                                                                                                                                                                                                                         Similarity
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                                                                                                                                            PTYNFAVAIDDHDMQISHVIR
                                                                                                                                                                        PSYSFARA---HDSEVQDIIR 19
                                                                                                                                                                                                                                                                                                                                 proteome.
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
NA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                     255
258
   (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae (strain ATCC BAA-255 / R6).
nicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                       AΑ;
                                                                STANDARD;
42,
42,
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259
258
55912
                                                                                                                                                                                                                        40.5%;
                                Created)
                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                      "KMSKS" REGION.
"KMSKS" REGION.
AIP (BY SIMILARITY).
                                                                                                                                                                                                                         Score 44.5;
Pred. No. 2
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                                                                 PRT;
                                                                                                                                             216
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud B., Durant L., Dussuurget O.,
A Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Charbit A., Chetouani F., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
A Gautier L., Mairournam A., Wata Vicente J., Ng B., Nedjari H.,
A Madueno E., Mairournam A., Mata Vicente J., Ng B., Nedjari H.,
A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Nachaman J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.";
Science 294:849-852(2001).
                                                                                             Query Match
Best Local &
                                                                                 Matches
                                                                                                                                                                                                             Librilist; LIN01197; -.

HAMMAP; MF 00203; -; 1.

InterPro; IPR003583; HHH 1.

InterPro; IPR0031843; UVTB/C.

InterPro; IPR0014791; UVTC.

InterPro; IPR0014791; UVTC.

InterPro; IPR00162; UVTC.

InterPro; IPR003055; UVTC.

InterPro; IPR00305; UVTC.

Pfam; PF001541; Exci endo_N; 1.

Pfam; PF001541; UVR; 1.

PF0DOm; PF005870; UVTC.

SMART; SM00465; GIYC; I.

SMART; SM00278; HhH1; 1.

INGREAMS; TIGR00194; UVTC; 1.

PROSITE; PS50164; UVTC.

PROSITE; PS50164; UVTC.

PROSITE; PS50165; UVTC.

1.
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MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LOCATION: Cytoplasmic (By 8
-:- SIMILARITY: Belongs to the uvrC family.
-:- SIMILARITY: Contains 1 UVR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; AD1582; AD1582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL596167; CAC96428.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: The UvrABC repair system catalyzes the recognition processing of DNA lesions. UvrC both incises the 5' and 3' silof the lesion. The N-terminal half is responsible for the 3' incision and the C-terminal half is responsible for the 5' incision (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Interacts with uvrB in an incision complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC system protein OR LIN1197.
                                                                                                                                                                                               response; Excision nuclease; DNA repair; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
                                                                                                                                                                                  excision;
               42
                                                                               Similarity
9; Conser
                               VPSYSFARAHDSEVQDIIRDII
VRSY-FSGTHDSKTQRLVQEIV
                                                                                                                                                  197
603 AA;
                                                                                 Conservative
                                                                                                                                                                                Complete proteome.
                                                                                                                                                  69302 MW;
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                                                                                               40.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UvrC protein) (Excinuclease ABC subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not removed.
                                                                                 7;
                                                                                                                                                                    Pred.
                                                                                                                 Score
                                                                                                                                                    8FA17669DB8EAFA1
                                               22
                                                                                   Mismatches
                                                                                                                  44.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                    BB
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                                                                                   5
                                                                                                                                                      CRC64;
                                                                                                                  Length 603;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration -
MBL outstation -
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RESULT 14
                                          Query Match
Best Local Similarity
                                                                                                                                                                                              Histifist; LM001234; -...
HAMAP; MF 00203; -; 1...
InterPro; IPR003583; HHH 1...
InterPro; IPR001943; UvrB/C...
InterPro; IPR001943; UvrC...
InterPro; IPR001162; UvrC.C...
InterPro; IPR000305; UvrC.N...
Pfam; PP01541; Exci. endo.N; 1...
Pfam; PP02151; UVR; 1...
ProDom; PD005870; UvrC.C; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UVRC LISMO
Q8Y7F0;
10-OCT-2003
10-OCT-2003
                                                                                                       SMART; SM00465; GIYC; 1.
SMART; SM00278; HhH1; 1.
TIGRAMS; TIGR00194; uvrC; 1.
PROSITE; P850151; UVR; 1.
PROSITE; P850164; UVRC 1; 1.
PROSITE; P850165; UVRC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glaser P., Frangell I., Buchrieser C., Rusniok C., Amend A., Glaser P., Frangell I., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget C., Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P., Gautier I., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I., Gomes I.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Matournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R. Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UvrABC system pr
UVRC OR LMO1234.
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                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes.
Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42,
10-OCT-2003 (Rel. 42,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
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                                                      SOS response; Excision nuclease;
DNA excision; Complete proteome.
DOMAIN 197 232 UVR.
                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL591978; CAC99312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      PIR; AB1229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Interacts wit similarity).
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the uvrC far
SIMILARITY: Contains 1 UVR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  incision and the C-terminal half is responsible for incision (By similarity).
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Rel. 42, Last annotation update)
protein C (UvrC protein) (Excinuclease ABC subunit
                                                                                                                                                                                                                                                                                                                                                        AB1229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                             ΑA;
                                              69315 MW;
 40.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uvrB in an incision
   Score 44.5;
Pred. No. 3
                                              E87D742AF5F3325B
                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
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Matches 8
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16-OCT-2001
16-OCT-2001
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YH75_ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavege A.R., Graham D.E., Kyrpides N.C., Pleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                    RPOC WE:
             15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical AF1775.
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Archaeoglobi;
Archaeoglobaceae; Archaeoglobus.
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                                                                                                                                                                                                                                                   Pfam; PF01979; Amidohydro 1; 1.
Hypothetical protein; Hydrolase; Complete proteome.
SEQUENCE 330 AA; 37069 MW; 525AD9F7F35A6FB1 CRC64;
                                                                                                                                                                                                                                                                                                                         EMBL; AE000980; AAB89475.1; -. PIR; F69471; F69471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the ATZ/TRZ family.
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                                                                                                                                                                                                                                                                                                             TIGR; AF1775;
  DNA-directed
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8; Conserv
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                                                                                                                                                                                                Conservative
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(Rel. 37, Created)
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(Rel. 37, Last amnotation (EC 2
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Pred. No.
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Query Match
Best Local Similarity
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InterPro; IPR007060; RNA_pol_Rpbl_3.
InterPro; IPR007060; RNA_pol_Rpbl_3.
InterPro; IPR007066; RNA_pol_Rpbl_4.
InterPro; IPR007081; RNA_pol_Rpbl_5.
InterPro; IPR0067081; RNA_pol_Rpbl_5.
InterPro; IPR006792; RNA_pol_Rpbl_1; 1.
Pfam; PP04997; RNA_pol_Rpbl_2; 1.
Pfam; PP04997; RNA_pol_Rpbl_2; 1.
Pfam; PF04998; RNA_pol_Rpbl_3; 1.
Pfam; PF04998; RNA_pol_Rpbl_4; 1.
Pfam; PF04998; RNA_pol_Rpbl_4; 1.
Pfam; PF04998; RNA_pol_Rpbl_5; 1.
SMART; SM00663; RPOLA_N; 1.
                                                                                                                POL3 DROME
PO4323;
PO4323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97016803; PubMed-8863429;
MOTSE R., Colling M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;
"Analysis of the beta' subunit of DNA-dependent RNA polymerase does
not support the hypothesis inferred from 16S rRNA analysis that
not support the hypothesis inferred from 16S rRNA analysis that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substrates.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Int. J. Syst. Bacteriol. 46:1004-1009(1996).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oenococcus oeni (formerly Leuconostoc (fast-evolving) bacterium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=46256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weissella hellenica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta' chain) (RNA polymerase beta' subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                              20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
20-MAR-1987 (Rel. 04, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Retrovirus related Pol polyprotein from transposon 17.6 (Contains:
Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49);
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                              Endonuclease).
                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; DNA-directed RNA polymerase; Transcription
Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta' chain.
SIMILARITY: Belongs to the RNA polymerase beta' chain family.
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                                                                                                                                                                                                                                          327
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Q9KWU6; 1HQM.
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Pred. No.
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EMBL outstation -
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Best Local
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InterPro; IPR001969; Asg
InterPro; IPR009007; Peg
InterPro; IPR001995; Peg
InterPro; IPR001584; Rve
InterPro; IPR000477; RVI
Pfam; PF000675; rve; 1.
Pfam; PF00077; rvp; 1.
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Nature 312:659-661(1984).
-!- CAȚALYȚIC ACTIVITY: N
SEQUENCE FROM NO...
STRAIN=MAFF303099;
STRAINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082950; PubMed=11214968; PubMed=11214968; PubMed=11214968; PubMed=112149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            098GV1;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X01472; CAA25702.1;
PIR; A03971; GNFF17.
MEROPS; A02.052; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85061628; PubMed=6209583;
Saigo K., Kugimiya W., Matsuo Y., Inouy
"Identification of the coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transposable element called 17.6.
-- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - i- MISCELLANEOUS: The open read transposable element called
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of the coding sequence for a transposable transcriptase-like enzyme in a transposable
                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                               298GV1;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endonuclease;
ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00141; ASP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                   Ubiquinone/menaquinone (EC 2.1.1.-).
UBIE OR MLR3165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSYPQAYEQEVESQIQDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSFARAHDSEVQDIIRDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspartyl protease; RNA-directed DNA polymerase; se; Transferase; Polyprotein; Transposable element 30 protease (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspprotease AS.
Pept A_acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%;
36.8%;
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Rve.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.6\pol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C893F5C4A7E1F091 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inouye S., Yoshioka K., uence for a reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frame is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258
                                                      Kawashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic
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                                                      Kato T., Sasar
ima K., Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            element
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MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
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Y326_M
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP003001; BAB50115.1; -.

HAMAP; MF_01813; -; 1.

InterPro; IPR001601; Methyltransf.

InterPro; IPR001601; Methyltransf.

InterPro; IPR004034; Ubi/men Metransf.

InterPro; IPR004033; UbiE/COQ5_Metrf.

Pfam; PF01209; Ubie methyltran; 1.

PROSITE; PS01183; UBIE 1; 1.

PROSITE; PS01183; UBIE 2; 1.

Menaquinone biosynthesis; Ubiquinone biosynthesis; Transferase;

Methyltransferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kishida Y., Kiyokawa C., Kohara M.,
Mochizuki Y., Nakayama S., Nakazaki
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                           MYCGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome structure of the Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE

    -!- SIMILARITY: Belongs to the ubiB family.

STRAIN=ATCC 33530 / G-37;

MEDLINE=$6026346; PubMed=*7569993;

MEDLINE=$6026346; PubMed=*7569993;

Praser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Pleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.

Pritchman J.I., Weidman J.F., Small K.V., Sandusky M., Fuhrmann

Mguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                      01-FEB-1996
10-OCT-2003
                                                                                                                                                                                                                                                                  01-FEB-1996
                                                                                                                                                                                                                                                                                 P47568;
                                                                                                                                                                                                                                                                                               Y326_MYCGE
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=2097;
                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                           Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DMKH2) to menaquinone (MKH2) and the conversion of 2-polyprenyl-6-methoxy-1,4-benzoquinol (DDMCH2) 2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol (DMCH2) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g-adenosyl-L-homocysteine + menaquinol
PATHWAY: Menaquinone biosynthesis; last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methoxy-1,4-benzoquinol = S-adenosyl-L-homocysteine
polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol.
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Ubiquinone biosynthesis
                                                                                                                                                                                                                                                                                                                                                                        15
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
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                                                                                                                                                                                           genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AA;
                                                                                                                                                                                                                      (Rel. 33,
(Rel. 42,
1 UPF0230
                                                                                                                                                                                                                                                                  Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                       33,
33,
42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                39.1%;
                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                       Last sequence u
                                                                                                                                                                             Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                           MG326
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9909682B726B2828
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                    295
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-mib.ch/announce/
                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      symbiotic bacterium
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steine + 2-
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Sugimoto
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                                                                                Kelley J.M.,
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hodgkinson C.A., Moore K.J., Nakayama A., Steingrimsson E., Copeland N.G., Jenkins N.A., Arnheiter H.;
"Mutations at the mouse microphthalmia locus are associated with defects in a gene encoding a novel basic-helix-loop-helix-zipper protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 270:397-403(1995)
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PIR; A64236;
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Hypothetical protein; Complete proteome.
SEQUENCE 295 AA; 33413 MW; 04610881C0F841EE CRC64;
                                                                          Steingrimsson E., Moore K.J., Lamoreux M.L., Ferre-D'Amare Burley S.K., Sanders Zimring D.C., Skow L.C., Hodgkinson C. Arnheiter H., Copeland N.G., Jenkins N.A.;
                                                                                                                                                                                                                                                                                                      Magnusdottir R., Gunnarsson G.J., Sweet H.O., Copeland N.G., Jenkins N.A., Steingrimsson E.; "Genomic, transcriptional and mutational analysis of the mouse microphthalmia locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/Sv; TISSUE=Heart;
MEDLINE=20253112; PubMed=10790403;
Hallsson J.H., Favor J., Hodgkinso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003797; Dept. Pfam; PF02645; DUF194;
"Molecular basis of mouse microphthalmia (mi) mutations helps explain their developmental and phenotypic consequences.";
Nat. Genet. 8:256-263(1994).
                                                                                                                                                           STRAIN=C57BL/6; TISSUE=Heart, and MEDLINE=95179171; PubMed=7874168;
                                                                                                                                                                                                                                                                               Genetics 155:291-300(2000).
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                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A. (ISOFORMS H AND M),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Melanocyte;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74:395-404(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE SPLICING,
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Pred. No.
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Sciurognathi; Muridae;
                                                                                                                                                                                                 and Melanocyte;
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Sweet H.O., Cope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M1),
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                                                                                                                                                                                                                              AND VARIANTS
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; Murinae; Mus
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MEDLINE=94012591; PubMed=8407885;
Hughes M.J., Lingrel J.B., Krakowsky J.M., Anderson K.P.;
"A helix-loop-helix transcription factor-like gene is located
mi locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene: the loss of a single Mitf isoform responsible pigmentary defect and inner ear deafness."; Hum. Mol. Genet. 8:1431-1441(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amae S., Fuse N., Yasumoto K.-I., Sato S., Ya
Udono T., Durlu Y.K., Tamai M., Takahashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 345-392 FROM N.I
STRAIN=C57BL/6; TISSUE=Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98321192; PubMed=9647758;
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Yajima I., Sato S., Kimura T., Yasumoto K.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT MI-BW.
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eye, ear, skin and heart. Isoform M is expressed and also in the embryonic and adult heart while i are more widely expressed.

PTM: PHOSPHORYLATION AT SER-405 SIGNIFICANTLY ENHITO BIND THE TYROSINASE PROMOTER (BY SIMILARITY).

DISEASE: DEFECTS IN MITTE ARE THE CANTON OF THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE CANTON AND THE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retinal pigment epithelium.
SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Binds DNA in the form of homodimer or heterodimer with either TFE3, TFEB or TFEC.
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                               IsoId=008874-9; Sequence=VSP 002130, VSP 002134 TISSUE SPECIFICITY: In the adult, expressed at his heart, skin, skeletal muscle, intestine, stomach, lung, spleen and brain. In the embryo, expressed
                                                                                                                                                                                                                             Name=M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived melanocytes, mast cells, osteoclasts and optic cup-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (5'-CACGTG-3') found in the tyrosinase promoter. Plays a Cr.
                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q08874-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q08874-2;
                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q08874-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q08874-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q08874-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I., Sato S., Kimura T., C.R., Yamamoto H.;
                                                                                                                                                                                                                                                   IsoId=Q08874-8;
                                                                                                                                                                                                                                                                                          IsoId=Q08874-7;
                                                                                                                                                                                                                                                                                                                                     IsoId=Q08874-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268:20687-20690(1993).
                                                                                                                                                                                                                                                                                      Sequence=VSP_002129, VSP_002133;
                                                                                                                                                                                                                                               Sequence=VSP_002130;
                                                                                                                                                                                                                                                                                                                                 Sequence=VSP_002129, VSP_002132,
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         SIGNIFICANTLY ENHANCES
(BY SIMILARITY).

B CAUSE OF MICROPHTHALMI
                                                                                                                    expressed at high levels in the estine, stomach, kidney, ovary bryo, expressed in developing M is expressed in melanocytes
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                                                                                                                                                                                                             VSP 002134;
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               MICROPHTHALMIA
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                                                             ABILITY
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CONDITION CHARACTERIZED BY LOSS OF PIGMENTATION; REDUCED EYE SIZE; FAILURE OF SECONDARY BONE RESORPTION; REDUCED MUMBERS OF MAST CELLS; RARLY ONSET OF DEARWASS, AND WHICH GIVES RISE TO A NUMBER OF DIFFERENT PHENOTYPES. ANONG THEM, MICROPHTHALMIA-FYELESS WHITE (MI-EW) HAS A NORMAL APPEARANCE AT THE HETEROZYGOUS STATE, BUT SHOWS WHITE COAT; EYES ALMOST ABSENT AND EYELDS NEVER OPEN AT HOMOZYGOSITY MICROPHTHALMIA-BLACK AND WHITE SPOT (MI-BWS) IS NORWAL AT HETEROZYGOSITY, AND PRESENTS WHITE SPOT (MI-BWS) IS NORWAL AT HETEROZYGOSITY, AND PRESENTS WHITE SPOTS AND BLACK EYES AT HOMOZYGOUS STATE. MICROPHTHALMIA-BLACK AND WHITE SPOTS AND BLACK EYES AT HOMOZYGOSITY, AND PRESENTS WHITE SPOTS AND BLACK EYES AND HOMOZYGOSITY, AND DERMIS SPOTS ON TOES, TAIL AND BLACK EYES AND HOMOZYGOSITY, AND DERMIS SMALLER THAN NORMAL, AND INNER EAR DEFECTS AT HETEROZYGOSITY, AND DERMIS SMALLER THAN NORMAL, HENOTYPE AT HETEROZYGOSITY, BUT SHOWS GRADUAL DEPIGMENTATION OF COAT, SKIN AND EYES; AND RETINAL DEGENERATION AT HOMOZYGOSITY.

MICROPHTHALMIA-SPOTTED (MI-SP) SHOWS NORMAL PHENOTYPE; AT HOMOZYGOSITY, HOWEVER, TYROSINASE ACTIVITY IN SKIN IS REDUCED. MICROPHTHALMIA-SPOTTED (MI-SP) SHOWS NORMAL PHENOTYPE; AT MICROPHTHALMIA-SPOTTED (MI-SP) SHOWS WHITE COAT; EYES OF REDUCED SIZED AND POSSIBLE MILD OSTEOPOROSIS AT HOMOZYGOSITY.

MICROPHTHALMIA-SPOTTED (MI-SP) SHOWS WHITE COAT; EYES OF REDUCED SIZE AND UNDIGNEMINED AS POSSIBLE MILD OSTEOPOROSIS AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT HOMOZYGOSITY. MICROPHTHALMIA-BLACK AT 
SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pumarate hydratase class I, aerobic (EC 4.2.1.2)
FUMA OR B1612 OR C2004.
Escherichia coli, and
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STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G.
Welch R.A., Buckles E.L., Liou S.-R.,
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STRAIN=K12;
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MEDLINE=84221385; PubMed=6328431;

Miles J.S., Guest J.R.;

"Complete nucleotide sequence of the fumarase gene fuma,

Escherichia coli.";

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Science 277:1453-1474(1997).
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
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IDENTIFICATION OF THE STRUCTURAL GENE.
MEDLINE=86142617; PubMed=3005475;
Guest J.R., Miles J.S., Roberts R.E., Woods S.A.;
"The fumarase genes of Escherichia coli: location and discovery of a new gene (fumC).";
J. Gen. Microbiol. 131:2971-2984(1985).
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STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
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BINDING
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"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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PROSITE; PS00163; FUMARATE LYASES; 1.
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ENZYME REGULATION: SUBJECT TO AEROBIC RESPIRATORY CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long as its content is in and this statement is not removed. Usaga by requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requires a light of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement of the requirement 
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      IRON-SULFUR (4FE-4S)
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                                                                                                               (4FE-4S)
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RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Hobeisel J., Zimmermann W., Wedler H., Ridley P., RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., RA Langham S.-A., McCullagh B., Bilham I., Robben J., Vandenbussche F., RA Hangham S.-A., McCullagh B., Bilham I., Robben J., Vandenbussche F., RA Holzer E., Brandt J., Optock M., Bastlaens I., Aert R., Defoor E., RA Holzer E., Berndt A., Peters S., Van Staveren M., Dirkse W., RA Holzer E., Rein Lankhorst R., Rose M., Hauf J., Koetter P., RA Mcoifman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Gielen J., Villarroel R., De Clercq R., RA Clark L., Doggett J., Hall S., Kay M., Lennard M., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard M., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard M., McLay K., Mayes R., RA Dose S., de Haan M., Marse A.C., Schaefer M., Meller-Auer S., RA Dose S., de Haan M., Marse A.C., Schaefer M., Meller-Auer S., RA Gabel C., Puchs M., Fartmann B., Granderath K., Daumer D., Herzl A., RA Gabel C., Puchs M., Fartmann B., Granderath K., Daumer D., Herzl A., RA Gabel C., Puchs M., Fartmann B., Granderath K., Daumer D., Herzl A., RA Gabbons T., Weber N., Schnidt W., Lecharny A., Labourg S., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Francs P., Bielber R., Berger C., Monfort A., Casacuberta E., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., RA Frishman D., Hasse D., Lenck K., Mewes H.-W., Stocket S., RA Frishman D., Bevan M., Wilson R.K., de la Bastide M., Habbermann K., RA Frishman D., Bevan M., Wilson R.K., de la Bastide M., Habbermann K., RA Schnach M., Murray J., Sheet P., Cordes M., Abu-Threideb J., Ra Frishman D., Bariley D., Fulton B., Miller N., Greco T., Kemp K., RA Ra Frishman D., Mardis E., Dante M., Pepin K., Johnson D., RA Minx P., Beriley D., Falton S., Marews S., Geisel C., Layman D., Layman D., Johnson D., Johnson D., Mardis S., Dante M., Pepin K., Hillier L.W., Johnson D., Mardis S., Dante M., Pepin K., Hiller L.W., Mardis D.,
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Best Local &
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable WRKY transcription factor 20 (WRKY DNA-binding protein WRKY20 OR AT4G26640 OR TISN24.90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=cv. Columbia, TISSUE=Flower;
Ulker B., Kushnir S., Somssich I.E.;
"Arabidopsis thaliana transcription factor WRKY20.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kreis M., Delseny M., Puigdomenech P., Watson M., So
Reichert B., Portetelle D., Perez-Alonso M., Boutry
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MEDLINE=20083488; PubMed=10617198;
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RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.K., Jones T., Kawai J.,
RA Khan S., Koesema E., Ishida J., Jiang P.K., Jones T., Kawai J.,
RA Khan S., Koesema E., Ishida J., Wallender B.K., Wong C., Yamamura Y.,
RA Khan S., Koesema E., Ishida J., Wallender B.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
Query Match
Best Local
                                                                                                                                                                                                                                                         EMBL; AF425837; AAL13050.1; -
EMBL; AL078465; CAB43860.1; A
EMBL; AL161565; CAB79519.1; A
EMBL; AY45892; AAK76566.1; -
EMBL; AY150436; AAN12978.1; -
ER; T08930; T08930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome.";
Science 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence and thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22954850; PubMed=14593172;
                                              CONFLICT
                                                                                                                                             DNA_BIND
                                                                                              VARSPLIC
                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                               Alternative
                                                                                                                                                                                               Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Transcription factor. Interacts specifically with the box (5'-(T)TGAC(C/T)-3'), a frequently occurring elicitor-responsive cis-acting element (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q93WV0-2; Sequence=VSP_007247, VSP_007248; Note=No experimental confirmation available; SIMILARITY: Belongs to the WRKY group I family. SIMILARITY: Contains 2 WRKY domains.
CAUTION: Ref.2 sequences differ from that shown du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative
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PF03106; WRKY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBOId=Q93WV0-1; Sequence=Displayed;
Note=No experimental confirmation a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302:842-846(2003).
 Similarity
                                                                                                                                                                                                              03106; WRKY; 2.
PS50811; WRKY; 2.
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Jn regu.
Pe splicing.
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                                                ΑĀ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences differ from that shown due to erroneous
                                                108
61033 MW;
                                                                                              76
 39.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing; Named isoforms=2;
                                                                                                                                                                                                DNA-binding;
                                                                                                                                                                                                                                                                                                           ALT_SEQ.
                                              Missing (in isoform 2).
/FTId=VSP 007247.
SNIK -> MILL (in isoform 2
/FTId=VSP 007248.
/FTId=VSP 007248.
Q -> R (IN REF. 3; AAK7656
Q -> G (179384AA4CEF0D9 CRC64;
   Score
Pred.
                                                                                                                                             WRKY 1.
   No.
DB
47;
                                                                                                                                                                                                Nuclear protein; Repeat;
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Gene 103:135-136(1991).
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-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
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Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
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Leucyl-tRNA synthetase
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396
462
579 AA;
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799 AA;
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(Rel. 42,
(Rel. 42,
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                                                                                   Conservative
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578
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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(EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
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    364
                                                                                                                                                                                                                                                                                  Protein biosynthesis; Ligase; ATP-binding;
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Pred. No.
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SUBSTRATE CARBOXYL (POTEN
; C46A90F6E97FCA5D CRC64;
                                                                                                         Score 43;
Pred. No.
                                                                                                                                                                                            "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                            "HIGH" REGION
                                                                                                                                                                          33B62E3CD73D06FE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oshima K., Kenri T., Furuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
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                                                                                                                                DB 1;
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                                                                                                                             Length 799;
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Matches
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Best Local
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10-OCT-2003
10-OCT-2003
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Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H., Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H., Miyaki C.Y., Furlan L.R., Camargo L.E.A., Ferro M.I.T., da Silva F.R., Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E., Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Cannavar F.S., Celestino A.V., Cachada A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T., de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XYLFT
                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoutation update)
Glycine dehydrogenase [decarboxylating] EC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCSP XYLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         decarboxylase)
                                                                                                                                                                                  EMBL; AB012555; AA028492.1; -. HAMAP; MF 00711; -; 1. InterPro; IPR003437; GDC-P.
                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylella fastidiosa (strain Temeculal / ATCC 700964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCVP OR PD0620
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a detween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kitajima J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanthomonadaceae; Xylella.
                                                                                                                                       Oxidoreductase; Pyridoxal phosphate; Co
BINDING 715 715 PYRIDOXAL
                                                                                                                                                                         Pfam; PF02347; GDC-P; 1.
                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fastidiosa.";
                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the govP family.
                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: The glycine cleavage system is composed of four proteins:
    969
                                                              Similarity 7; Conser
IPVEAYKEKGDSEIQDLIEE 988
                                 VPSYSFARAHDSEVQDIIRD 20
                                                                                                                            993 AA;
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Glycine cleavage system P-protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                            107646 MW;
                                                                              39.1%;
35.0%;
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                                                                9
                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                            hate; Complete proteome.
RIDOXAL PHOSPHATE (BY SIMILARITY).
BCC04E829C442F43 CRC64;
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    993
                                                                                , 88
                                                                                                                                                                                                                                                                                                                There are no
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                                                                                               Length 993;
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                                   outstation
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RESULT 27
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Best Local S
Matches
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
10-OCT-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ketoisovalerate oxidoreductase subunit vorA (EC 1.-.-) (VOR)
oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-
ferredoxin oxidoreductase alpha subunit).
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                                                                                                                                                                                                                   SYE MYCPN
P75114;
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PIR; B75047; B75047.
InterPro; IPR002880; POR_N.
InterPro; IPR009011; Transketo_C_like.
Pfam; PF01855; POR_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecon Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; "An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.";
Mol. Microbiol. 47:1495-1512(2003).

-i- SUBUNIT: Heterotetramer of one alpha, one beta, one delta a
                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Con
SEQUENCE 395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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MEDLINE=22511545; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ругососсив
                                 SERQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VORA_PYRAB
                         Herrmann R.;
                                                                                                               Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes;
                                                                                                                                                                               01-NOV-1997
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                  NCBI_TaxID=2104;
                                                                                                                                         GLTX OR MPN678 OR MP164.
                                                                                                                                                                   Glutamyl-tRNA
                                                                                                                                                                                                         01-NOV-1997
            "Complete sequence analysis
                                                                                                                                                        GluRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma chain.
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8; Conser
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(Rel. 35, Last seq
(Rel. 41, Last ann
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                                                                                                                                                                   synthetase
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                                                                                                                                                                   Last sequence update)
Last annotation update)
case (EC 6.1.1.17) (Glutamate--tRNA ligase)
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Pred. No. 3!
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                                                                                                                                                                                                                                  PRT;
             the
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                                                                                                                  Mycoplasmataceae; Mycoplasma
            genome
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                                     Pirkl E.,
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              the
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              bacterium
                                        Li B.-C.,
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              Mycoplasma
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Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                           HXTD YE P42833;
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BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 24:4420-4449(1996).
-!- CATALYTIC ACTIVITY: ATP + L-Glutamate + tRNA(Glu) = AMP + diphosphate + L-glutamy1-tRNA(Glu).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAD; MF_00022; -; 1.
InterPro; IPR004527; GltX bact.
InterPro; IPR000924; Glt TRNA-synt lc.
InterPro; IPR000925; tRNA-synt bind.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_Ic; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                            YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; 873490; 873490.
HSSP; P27000; 1GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000017; AAB95812
                                                                                                       STRAIN=S288c / FY1676;
MEDLINE=96076632; PubMed=7502583;
Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.;
Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.;
Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.;

"Sequencing analysis of a 24.7 kb fragment of yeast chromosome identifies six known genes, a new member of the hexose transpor family and ten new open reading frames.";

Yeast 11:1077-1085 (1995).

-I- FUNCTION: PROBABLE GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGR00464; gltX_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE I;
Aminoacyl-tRNA synthetase; Protein b
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00987; TRNASYNTHGLU
                                                                                           SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                            YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 IATYNFAVVIDDHDMEITDVLR 213
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252
255
484 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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256
255
55621,
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                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6,
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ATP (BY SIMILARITY)
; FD7B7F4742B09A50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                            membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                               540
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                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                 8
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MBL outstation -
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MAD2_YI
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Best Local
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PROSITE; PS50850; MFS; 1.

PROSITE; PS00216; SUGAR TRANSPORT 2; 1.

PROSITE; PS00217; SUGAR TRANSPORT 2; 1.

PROSITE; PS00217; SUGAR TRANSPORT 2; 1.

PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
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DOMAIN
TRANSMEM
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TRANSMEM
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                                                                                                                        MAD2 1
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TRANSMEM
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TRANSMEM
                                                           P40958;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation updat
Mitotic spindle checkpoint component MAD2 (MAD2 OR YJL030W OR J1256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0171; SUGRTRNSPORT.
TIGREAMS; TIGR00879; SP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00083; sugar_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
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                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S0005262; HXT14
                                                                                                                        YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z46259; -; NOT ANNOTATED_CDS.
Z71595; CAA96250.1; -.
                                                                                                                                                                            277
                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                             VPS--YSFAR-----AHDSEVQDIIRDII 22
FROM N.A
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399
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77
120
141
147
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                                                                                                                        STANDARD;
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167
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461
                                                                                                                                                                                                                                                             60978 MW;
                                                                                                                                                                                                                            38.6%;
                                                                                                                                                                                                                   Score 42.5; I
Pred. No. 54;
3; Mismatches
                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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10 (POTENTIAL)
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MAD2 (Mitotic MAD2
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                                                                                                                                                                                                                                        Length 540;
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                                                                       protein)
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RESULT 30
ANPC BNPC
ID ANPC
DT 01-U7
DT 01-U0
DT 01-U0
DT 28-FI
DB Atria
DB (ANPB
GN NPR3
OS Bos t
OC Mammu
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                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Pohl T.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Reedback control that prevents cells with incompletely assembled spindles from leaving mitosis.
-!- SUBUNIT: The spindle checkpoint complex is composed of MAD1, MAD2 and MAD3. It interacts with CDC20.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
-!- SIMILARITY: Contains 1 HORMA domain.
                                                                                                                                                                                                                                                                                                                                                                                                        SGD; S0003567; MAD2.
GO; GO:0000778; C:condensed nuclear chromosome kinetochore;
GO; GO:0005643; C:nuclear pore; IDA.
GO; GO:0007094; P:mitotic spindle checkpoint; IGI.
InterPro; IPR003511; DNAbind_HORMA.
                                        ANPC BOVIN STANDARD; PRT; 537 AA.

P10730; P20644;
01-JUL-1989 (Rel. 11, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Atrial natriuretic peptide clearance receptor precursor (ANP-C)
(ANPRC) (NPR-C) (Atrial natriuretic peptide C-type receptor).

NPR3 OR ANPRC.
                                                                                                                                                             BOVIN
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50815; HORMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z49305; CAA89321
PIR; S48302; S48302.
HSSP; Q13257; 1DUJ.
GermOnline; 141645; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Budding yeast Cdc20: a target of the Science 279:1041-1044(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hwang L.H., Lau L.P., Smith D.L.,
Hwang B.S., Amon A., Murray A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Feedback control of
Cell 66:519-531(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li R.,
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    Cell cycle; Mitosis; Nuclear protein.
DOMAIN 8 192 HORMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98128031; PubMed=9461437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTIONS
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 Eukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02301; HORMA;
                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U14132; AAA21385.1; -.
                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Havel C.,
                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                          ! Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                RAHDSEVQDIIRDII 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Aljinovic
| (SEP-1995)
                                                                                                                                                                                                                      KTHDDELKDYIRKIL
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                                                                                                                                                                                                                                                                                                                                      196 AA;
                              (Bovine).
                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of mitosis in budding yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1651172;
Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t G.;
                                                                                                                                                                                                                                                                                                                                        22284 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                           38.2%;
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the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                         Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                         EFE59916C5720644 CRC64;
                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spindle checkpoint."
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                                                                                                                                                                                                                                                                                4;
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      Pecora; Bovoidea;
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J. Biol.
[4]
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MEDIJINE=88243827; PubMed=2837487;

Fuller F., Porter J.G., Arfeten A.E., James J.M., Schilling J.W.,

Scarborough R.M., Lewicki J.A., Schenk D.B.;

"Atrial natriuretic peptide clearance receptor. Complete sequence functional expression of CDMA clones.";

J. Biol. Chem. 263:9395-9401(1988).
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between
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J. Biol. Chem. 269:8314-8318(1994).
-i- FUNCTION: EXCEPTOR FOR ATRIAL NATRIURETIC
GUANYLATE CYCLASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90088409; PubMed=2557006;
Uchida K., Mizuno T., Shimonaka M
Hagiwara H., Hirose S.;
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Itakura M., Iwashina M., Mizuno T., Ito T., F
"Mutational analysis of disulfide bridges in
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Biochem. J. 263:671-678(1989).
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MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO MITH GUANYLATE CYCLASE ACTIVITY (AND-AND AND-B) AND ONE (AND-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

SIMILARITY: TO AND-A AND AND-B RECEPTOR IN THEIR EXTRACELLULAR ANI TRANSMEMBRANE DOMAINS.
                                                                                                                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed
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D90372;
D90372;
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D90367;
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                                                                                                                                                                                      requires a
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  ; AAA30376.1; -. ; BAA14380.1; -. ; BAA14380.1; JOINED. ; BAA14380.1; JOINED. ; BAA14380.1; JOINED. ; BAA14380.1; JOINED.
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   004546 arabidopsis

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Q96bd8 homo sapien
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R EMBL; D13858; BAA02976.1; -.

R PIR; A39841; A39841.

PR G0; G0:0016757; Fitransferase activity, transferring glycosyl...; ]

PR G0; G0:0009250; P:glucan biosynthesis; IEA.

DR InterPro; IPR002479; CW binding.

DR InterPro; IPR003318; Glyco.hydro_70.

DR Pfam; PF01473; CW binding 1; 13.

DR Pfam; PF01473; CW binding 1; 13.

DR Pfam; PF02324; Glyco.hydro_70; 1.

KW Glycosyltransferase; Signal; Transferase.

KW Glycosyltransferase; Signal; Transferase.

FT SIGNAL 1 38 GLUCOSYLTRANSFERASE-I.

CHAIN 1500 AA: 175955 MW; C3C83A57CF3C2B0E CRC64;
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DNA Seq. 4:19-27(1993).
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01-OCT-2003
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STEAIN=MRRL B129;
MEDLINE=97136686; PubMed=8982063;
MODChois V., Willemot R.M., Remaud-Simeon M., Croux C., Monsan P.;
"Cloning and sequencing of a gene coding for a novel dextransucrase from Leuconostoc mesenteroides NRRL B-1299 synthesizing only alpha (6) and alpha (1-3) linkages.";
Gene 182:23-32(1996).

THUST: "TOTAL TANADAT"

FROMT. 182:23-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA and amino-acid sequences of water-insoluble-glucan synthetase produced from Streptococcus sobrinus ATCC 33478."; Ann. Kagoshima Univ. Dental School 16:23-29(1996). EMBL; D63570; BAA09792.1; -. PIR; A39841; A39841.
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InterPro; IPR002479; CW binding.
InterPro; IPR002318; Glyco_hydro_70.
Pfam; PF01473; CW binding I; 13.
Pfam; PF02324; Glyco hydro_70; 1.
SEQUENCE 1590 AA; 176058 MW; 9DF7A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0009250; P:glucan biosynthesis;
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW binding_1; 9.
Pfam; PF01473; Glyco_hydro_70; 1.
SEQUENCE 1290 AA; 145590 MW; 3555C:
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Bacteria; Firmicutes; Lactobacillales; Leuconostoc
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                                                         DSRR.
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   Bacteria;
                                 Leuconostoc
                                                                                       Dextransucrase
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17; Conserv
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Firmicutes; Lactobacillales;
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                                                                                       (TTEMBLIE1. 24, Created)
(TTEMBLIE1. 24, Last sequence update)
(TTEMBLIE1. 25, Last annotation update)
ase Dark (EC 2.4.1.5).
                              mesenteroides
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81.0%;
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Last sequence update)
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Pred. No. 2.
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         Leuconostoc
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"Gene encoding a dextransucrase
NRRL B-1501.";
                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0009250; P:glucan biosynthesis; InterPro; IPR002479; CW binding. InterPro; IPR003318; Glyco hydro_70. Pfam; PF01473; CW binding_1; 13. Pfam; PF02324; Glyco_hydro_70; 1. Glycosyltransferase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucosyltransferase from Leuconostoc mesenteroides NRRL
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250172; CAB76565.1; -.
GO; GO:0016757; F:transferase activity, transferring gly
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STRAIN=NRRL B-1355;
Arguello-Morales M.A., Rewillemot R.M., Monsan P.;
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Bacteria; Firmicutes; Lactobacillales; Leuconostoc
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  (TrEMBLrel. (TrEMBLrel.
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(TrEMBIrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
see (EC 2.4.1.5).
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    16,
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Pred. No. 0.00
3; Mismatches
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Pred. No. 0.00055;
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RESULT 8
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Best Local Similarity
Matches 15; Conserv
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G0; G0:0016757; F:transferase activity, t:
G0; G0:0009250; P:glucan biosynthesis; IE;
G0; G0:0009250; P:glucan biosynthesis; IE;
InterPro; IPR002479; CW binding.
InterPro; IPR00318; Glyco hydro 70.
Pfam; PF01473; CW binding_T; 13.
Pfam; PF02324; Glyco hydro 70; 1.
Glycosyltransferase; Transferase.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                           SEQUENCE THE STRAIN-HAREL B-1299;
STRAIN-HAREL B-1299;
MONChOIS V., Remaud-Simeon M., Monsan P.
MONChOIS V., Remaud-Simeon M., Monsan P.
"Cloning and sequencing of a gene codin
dextransucrase (DSRB) from Leuconostoc
synthesizing only a a(1-6) glucan.";
synthesizing only a a(1-6) glucan.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Leuconostoc mensenteroides B-742CB, a dextransucrase ger Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP294469; AAG38021.1; -. GO; GO:0009250; P:glucan biosynthesis; IEA. InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco hydro 70. Pfam; PF01473; CW_binding_T; 13. Pfam; PF01473; GW_binding_T; 13. Pfam; PF02324; Glyco hydro 70; 1. SEQUENCE 1508 AA; 168542 MW; E2FCFA0F87AE4F3A CRC64;
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01-JUN-2003 (TrEMBLrel.
Glucosyltransferase (EC
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01-JUN-2003
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Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
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EMBL; AF030129; AAB95453.1;
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Bacteria; Firmicutes; Lact
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B-742CB, a dextransucrase gene.";
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Pred. No. 0.00064;
3; Mismatches 4
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conostoc mesenteroides NRRL B-1299
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A Bhatnagar R., Singh D.K.S.;
Telenconostoc mesenteroides NRLL B-512F.";
Teuconostoc mesenteroides NRLL B-512F.";
I submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; UB1374; AAD10952.1; -.
R CO; GO:0009250; P:glucan biosynthesis; IEA.
R GO; GO:0009250; P:glucan biosynthesis; IEA.
R InterPro; IPR003479; CW binding.
R InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01473; CW_binding_l; 12.
Pfam; PF01473; CM_binding_l; 12.
Pfam; PF0324; Glyco hydro 70; 1.
SEQUENCE 1527 AA; 169709 MW; 1DFAFFA237C743398 CRC64;
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Q9ZAR4;
01-MAY-1999
Q8KRE1;
Q8KRE1;
01-OCT-2002
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InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF02324; Glyco_hydro_70; 1.
SEQUENCE 1016 AA; 110344 MW; 8896EI
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Bacteria; Firmicutes;
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STRAIN=NRRL B-512-F;
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Bacteria; Firmicutes; Lact
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Submitted (JAN-2001) to the RMBL/GenBank/DDBJ
EMBL; AV017384; AAG61158.1;
GO; GO:0016757; F:transferase activity, trans:
GO; GO:0009250; F:glucan biosynthesis; IEA.
InterPro; IPR0023479; CM_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CM_binding_1; 12.
Pfam; PF02324; Glyco_hydro_70; 1.
Transferase; Glycosyltransferase.
SEQUENCE 1527 AA; 169835 MM; F9D0DE220BD8.
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Q8KZL5;
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01-OCT-2003 (TrEMBLrel.
Dextransucrase DsrD (EC
                                                                                                                                                                                                           MEDLINE=21958684; PubMed=11960691;
Hanada N., Fukushima K., Nomura Y., Senpuk
Mukasa H., Shiroza T., Abiko Y.;
"Cloning and nucleotide sequence analysis
sobrinus gtfU gene that produces a highly
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01-JUN-2003
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          VPSYSFARAHDSEVQDIIRDII 22
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IPTYSFVRAHDSEVQTVIAKIV 578
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EMBL; A4430204; CAD22883.1; ---
GO; GO:0016757; F:transferase activity, ti GO; GO:0009250; P:glucan biosynthesis; IEF interPro; IPR0032479; CW binding.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01374; Glyco hydro 70; 2.
Pfam; PF02324; Glyco hydro 70; 2.
Transferase; Glycosyltransferase.
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"S.cricetus glucosyltransferase (gtfS and gtfT)
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ (
EMBL; AB026123; BAA77237.1; -.
EGO; GO:0046821; C:extrachromosomal DNA; IBA.
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Bozonnet S., Dols-Lafargue M., Fabre E.,
Mondan P., Willemot R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-JUN-2003 (TrEMBLrel. 24, Dextransucrase (EC 2.4.1.5)
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66.7%;
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; Score 75;
; Pred. No. |
3; Mismatch
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L; Mismatches
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Best Local S
Matches 14
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Q9LCH3;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q54178 PRELIMINARY;
Q54178; Q54247;
01-NOV-1996 (TremBLrel. 01, C
01-NOV-1996 (TremBLrel. 01, I
01-JUN-2003 (TremBLrel. 24, I
Glucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Purification, characterization, and molecular analysis of encoding glucosyltransferase from Streptococcus oralis."; Infect. Immun. 68:2475-2483 (2000).

EMBL; AB025228; BAA95201.; -.
GO; GO:0016740: Fitzensfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0009250; P:glucan biosynthesis; InterPro; IPR002479; CW binding. InterPro; IPR0032479; CW binding. InterPro; IPR003218; Glyco_hydro_70. Pfam; PF01473; CW binding_1; 16. Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016740; F:transferase activity; GO:0009250; P:glucan biosynthesis: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus.
MEDLINB=92276337; PubMed=1534326;
Sulavik M.C., Tardif G., Clewell !
"Identification of a gene, rgg, w
                                                                                                                                                                          STRAIN=CHALLIS;
MEDLINE=96157084; PubMed=8586195;
Vickerman M.M., Sulavik M.C., Clewell D.B.;
"Molecular analysis of Streptococcus gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20231779; PubMed=10768934; Pujiwara T., Hoshino T., Ooshima T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
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                                                                     SEQUENCE OF 1-96 FROM N.A. STRAIN=CHALLIS;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                       Streptococcus gordonii
Bacteria; Firmicutes; I
                                                                                                                                                                                                                                                                                                                                                                                                                       GTFG
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                                                                                                                                                              phase
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29390;
                                                                                                                                      Dev. Biol. Stand.
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                                                                                                                                                              variants."
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                     Tardif G., Clewell D.B.;
                                                                                                                                        85:309-314(1995)
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                                                                                                                                                                                                                                                                                                                                                                       i Challis.
Lactobacillales;
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24,
    rgg, which
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Pred. No. 0.02
2; Mismatches
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    regulates
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                                                                                                                                                                                                                                                                                                                                                                         Streptococcaceae;
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       expression
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EMBL, M89776; AAA26969.1; -.
EMBL, B41898; B41898.
PIR; B41898; B41898.
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gordonii Challis.";
J. Bacteriol. 174:39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glucosyltransferase S procursor (BC 2.4.1.5) (GTF) (Dextransucrase)
                                                                                                                                                                                                                                                                                            Glucosyltransferase genes in Streptococcus salivarius ATCC 25:
J. Gen., Microbiol. 137:2577-2593 (1991).
I. FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THE PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BETHEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
I- CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL) (N)
FRUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL) (N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus salivarius
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                                                                                                                EMBL; Z11872; CAA77898.1; -.
EMBL; Z11873; CAA77901.1; -.
EMBL; M64111; AAA26897.1; -.
PIR; S22737; S22737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92148377; PubMed=1838391;
Giffard P.M., Simpson C.L., Milward C.P., Jacques N.A.;
"Molecular characterization of a cluster of at least tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Sucrose 6-glucosyltransferase).
                          GO; GO:0016757; F:transferase activity, GO; GO:000955; F:glucan biosynthesis; Interpro; IPR002479; CW binding.
Interpro; IPR003318; Glyco_hydro_70.
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BL; U12643; AAC43483.1; -.
                                                                                                                                                                                                        DISEASE: DENTAL CARIES.
SIMILARITY: TO REGIONS OF BARLEY AND ALPHA AMYLASES AND RABBIT GLYCOGEN PI
                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: EXTRACELLULAR.
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       CW_binding
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70.0%;
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       o_hydro_70.
_1; 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcaceae;
                                                                            IEA.
                                                                                                                                                                                                               ND BACILLUS AMYLOLIQUEFACIENS PHOSPHORYLASE.
                                                                                                 transferring glycosyl.
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RESULT
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Q55264
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Best Local S
Matches 14
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Best Local
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068542;
01-AUG-1998
01-AUG-1998
01-JUN-2003
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SEQUENCE
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Transferase; Glycosyltransferase;
SIGNAL 1 42 POTEN
                                                                                                                                                                                                           Q55264;
Q55264;
01-NOV-1996
01-NOV-1996
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1998) to the EMBL/GenBank
EMBL; AF049609; AACOS156.1; -.
PIR; T30552; T30552.
GO; GO:0016740; F:transferase activity;
GO; GO:0009250; P:glucan biosynthesis; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus.
NCBI_TaxID=1304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus salivarius
SEQUENCE FROM N.A.
MEDLINE=95122197; PubMed=7822030;
Simpson C.L., Giffeard P.M., Jacque
"Streptococcus salivarius ATCC 255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase.
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                                                                                                                                    Streptococcus salivarius.
Bacteria; Firmicutes; Lac
                                                                                                                                                                                           Glucosyltransferase
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                                                                                                                Streptococcus
                                                                                            NCBI_TaxID=1304;
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(TrEMBLrel.
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    Giffard P.M., Jacques N.A.; salivarius ATCC 25975 poss
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176480 MW; 24B77869E152B707
                                                                                                                                                                                             precursor
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70.0%;
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Last annotation updat
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Pred. No.
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Last
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Pred. No. 0.049;
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annotation update)
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        роввеввев
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RESULT
Q9RE05
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"S. cricetus glucosyltransferase (gtfs and gtfT) ge
"S. cricetus glucosyltransferase (gtfs and gtfT) ge
submitted (MAR-1999) to the EMBL/GenBank/DDBJ dat
EMBL, AB026123; BAA77236.1; -

GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:009250; P:glucan biosynthesis; IEA.
GO: GO:009250; CW binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW binding.]; 9.
Pfam; PF02324; Glyco_hydro_70; 1.
Plasmid.
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
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Best Local
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GO; GO:0009250; F:glucan biosynthesis; IEA
InterPro; IPR002479; CM binding.
InterPro; IPR003318; Glyco hydro 70.
Pfam; PF01473; CM binding 1; 7.
Pfam; PF02324; Glyco hydro 70; 1.
Signal; Transferase.
SIGNAL 1 35 POTENTIAL.
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Q9WXJ4;
01-NCV-1999
01-NCV-1999
01-JUN-2003
                              Q9RE05;
Q9RE05;
01-MAY-2000
01-MAR-2001
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                             STRAIN=HS-6;
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
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 Leuconostoc
                    01-MAY-2000 (TrEMBirel. 13, Created)
01-MAR-2001 (TrEMBirel. 16, Last sequence update)
01-WIN-2003 (TrEMBirel. 24, Last annotation updat
Alternansucrase (EC 2.4.1.140).
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1333;
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1449 AA;
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(TrEMBLrel.
(TrEMBLrel.
 mesenteroides
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                                                                           PRELIMINARY;
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                                                                                                                                                                                 62.7%;
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12,
24,
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Last annotation update)
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                                                                                                                                                                        Score 69; DB
Pred. No. 0.06
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
GLUCOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                           PRT;
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                                  update)
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RESULT 21
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1996 (TrEMBLrel. 24, Last annotation update)
O1-UN-2003 (TrEMBLrel. 24, Last annotation update)
O1-ONVItransferase I (EC 2.4.1.5) (GTF) (Dextransucrase)
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MEDITINE 2148377; pubMed=1838391;

Milled P.M., Simpson C.L., Milward C.P., Jacques N.A.;

Molecular characterization of a cluster of at least two

Molecular characterization of a cluster of at least two

glucosyltransferase genes in Streptococcus salivarius ATCC 25975.";

J. Gen. Microbiol. 137:2577-2593(1991).

-I- PUNCTION: PRODUCTION OF BETRACELIULAR GLUCANS, THAT ARE THOUGHT

-I- PUNCTION: PRODUCTION OF EXTRACELIULAR GLUCANS, THAT ARE THOUGHT

-I- PUNCTION: PRODUCTION OF BETRACELSULAR GLUCANS, THAT ARE THOUGHT

-I- PUNCTION OF BACTERIAL CELLS AND FOOD DEBRIS.

AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
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InterPro; IPR002479; GW_binding-70.
Pfam; PP01473; CW_binding_1; 11.
Pfam; PP02324; Glyco hydro 70; 1.
Glycosyltransferase; Transferase.
SEQUENCE 2057 AA; 228987 MW; 62BCE9
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Arguello-Morales M.A.,
Willemot R.M., Monsan |
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EMBL; AJZ50173; CAB65910.2; -.

GO; GO:0016757; F:transferase activity, transferring glycosyl. ...
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Pred. No. 0.15;
3; Mismatches
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GO; GO:0009250; F:glucan biosynthesis; IE
InterPro; IPR004829; CSurface antigen.
InterPro; IPR002479; CW_binding.
InterPro; IPR00318; Glyco hydro 70.
Pfam; PF01473; CW_binding_I; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
ProDom; PD153432; CSurface_antigen; 1.
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EMBL; L35928; AAC41413.1; -.
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01-FEB-1997 (TrEMBLrel.
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SEQUENCE
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                                                       Hypothetical
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Q9ZIX9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
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Submitted (MAY-1997) to the
EMBL; AF006036; AAD01254.1;
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Hypothetical protein (Fragment).

Borrelia burgdorferi (Lyme disease spirochete).

Spirochaetes; Spirochaetales; Spiroch
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        Lengeler K.B., Wang P., Cox G.M., Perfect J.R., Heitman J.; "Identification of the MATa mating-type locus of Cryptococcus neoformans reveals a serotype A MATa strain thought to have be
                                                                                                                                                                SEQUENCE OF 940-1554 FROM N.A. STRAIN=H99;
                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; I
Tremellomycetidae;
NCBI_TaxID=178876;
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Eukaryota; Fungi; Basidiomycota;
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01-MAR-2003
                                                                                                                              MEDLINE=20570501; PubMed=11121047;
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34 NWARAHDQSLDDVVQEIL 51
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108 AA; 12030 MW; 589F5770326C0DBF
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(TrEMBLrel. 10,
(TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Tremellales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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Pred.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                          Hymenomycetes; Heterobasidiella Fremellaceae; Filobasidiella
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                              Heterobasidiomycetes;
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RESULT
Q8J0W2
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Best Local S
Matches 9
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InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
Pfam; PP01843; DIL; 1.
Pfam; PP01843; DIL; 1.
Pfam; PP00612; IQ; 6.
Pfam; PP00053; myosin_head; 1.
PRINTS; PR001935; myosin_head; 1.
SMART; SM00015; IQ; 6.
SMART; SM00015; IQ; 6.
SMART; SM000142; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extinct.";
Proc. Natl.
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                                                                                                                                                                                                                                               Q8J0W2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lengeler K.B., Fox D.S., Fraser J.A., Allen A., Forreste
Dietrich F.S., Heitman J.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=H99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=H99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lengeler K.B., Fox D.S., Fraser J.A., Allen A., Dietrich F.S., Heitman J.;
"Mating-type locus of Cryptococcus neoformans: of sex chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22343086; PubMed=12455690;
Lengeler K.B., Fox D.S., Fraser J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Eukaryot. Cell 1:704-718(2002).
EMBL; AF542531; AAN75723.1; -.
GO; GO:0016459; C:myosin; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity;
InterPro; IPR002710; DIL.
                                                                                             STRAIN=JEC21;
MEDLINE=22343086; PubMed=12455690;
----~ FOX D.S., Fraser J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryot. Cell 1:704-718(2002)
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                                                               Lengeler K.B., Fox D.S., Fraser J.1 Dietrich F.S., Heitman J.; "Mating-type locus of Cryptococcus of sex chromosomes.";
                                                                                                                                                                 Cryptococcus neoformans var. neoformans.
Bukaryota; Fungi; Basidiomycota; Hymenom
Tremellomycotidae; Tremellales; Tremella
                                                                                                                                                                                                               01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                     01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                  1253
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d (JAN-2002)
                                                                                                                                                                                                                                                                                                                 VPGYDFSNGHDSDWRGYIR 1271
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                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                   Fox D.S., ri
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                                                                                                                                                                   Basidiomycota; Hymenomycetes; Tremellales; Tremellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                       174915 MW;
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Last
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                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                     Score 50;
Pred. No.
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                         IEA.
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                                                                                                                                                                    Hymenomycetes; Heterobasidiomycetes; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                               sequence up
                                                                              neoformans:
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                                                                                                   Allen A.,
                                                                                                                                                                                                                                                                                                                                                                       78;
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RESULT 28
Q8R6U3
Q8R6U
ID Q8R6U
AC Q8R6U
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT NEMBI

PRELIMINARY,

PRT;

449

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Q8R6U3 Q8R6U3; Q1-UUN-2002 Q1-UUN-2002 Q1-UUN-2003 Membrane prot NLPD6 OR TTE2

2002 (TrEMBLrel. 21, Created)
2002 (TrEMBLrel. 21, Last sequence update)
2003 (TrEMBLrel. 24, Last annotation update)
2014 proteins related to metalloendopeptidases.
217TTE2691.

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RESULT 27
Q8A338
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Matches 8
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Pfam; PF00612; IQ; 6.

Pfam; PF00063; myosin_head; 1.

PRINTS; PR00133; MYOSINHEAVY.

PRODOM; PD000355; myosin_head; 1.

SMART; SM00015; IQ; 6.

SMART; SM00242; MYSC; 1.

SMART; SM00242; MYSC; 1.

SMART; SM00242; MYSC; 1.

SMART; SM00242; MYSC; 1.
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01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1)
SEQUENCE FROM N.A.
STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5250858; PubMed=1263928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8A338;
                                                                                                                                                                                                                                                                                                     EMBL; AE016939; AA078223.1; ...
GO; GO:0008677; F:2-dehydropantoate 2-reductas
GO; GO:0000036; F:acyl carrier activity; IEA.
GO; GO:0000036; P:fatty acid biosynthesis; IEA
GO; GO:000623; P:fatty acid biosynthesis; IEA
GO; GO:0006206; P:pyrimidine base metabolism;
InterPro; IPR003227; GDBH C like.
InterPro; IPR003231; Acyl carrier.
InterPro; IPR003231; Acyl carrier.
InterPro; IPR003710; ApbA.
                                                                                                                                                                                                                                    Pfam; PF02558; ApbA; 1.
ProDom; PD000887; Acyl_carrier; 1.
TIGRFAM8; TIGR00745; apbA_panE; 1.
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Chiang H.C., Hooper L.V., Gordon J.I.;
R genomic view of the human-Bacteroides
Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=818;
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Bacteroidaceae; Bacteroides
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InterPro; IPR001609; myosin_head.
                                                                                                                                                                                         SEQUENCE 303 AA;
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                                          ARAHDSEVODIIRDII
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                                                                                                                      Score 47;
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RESULT 29
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InterPro; IPR002486; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-MB4 / JCM 11007;
MEDLINE-21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu
Chen Y., Xue Y., Xu Y., Lai X., Huang L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis g
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pacceria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Enterobacter.
NOBI TATTOLICA
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                                                                                                                                          SEQUENCE
                                                                                                                                                              SIGNAL
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PROSITE; PS0012
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SYSFARAHDSEVQDIIRD 20
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                                                                                                                                                                             Signal.
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57922 MW;
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Pred. No. 60;
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Q8G5W2;
01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                     to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002)

EMBL; AB014710; AAN24703.1;

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000403; F:ATP dependent DNA helicase activ

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0004386; F:helicase activity; IEA.

GO; GO:0006281; P:DNA tepah; IEA.
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                                                                                                                                                                                                                                              Pfam; PF00580; UvrD-helicase; 1.
Helicase; Complete proteome.
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                                                                                                                                                                                                                                                                                                    InterPro; IPR000212; UvrD-helicase.
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881 AA; 96319 MW;
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TrEMBLrel. 25,
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PRIOR FILLING DATE: 1995-06-07
PRIOR PEPPLICATION NUMBER: 09/009,620
PRIOR PPPLICATION NUMBER: 09/485,243
PRIOR PPLICATION NUMBER: 09/485,243
PRIOR PILLING DATE: 1995-06-07
PRIOR PILLING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/008,172
PRIOR FILLING DATE: 1995-01-16
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GENERAL INFORMATION:
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EARLIER
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
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EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1996-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
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EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 08/485,243
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
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TITLE OF INVENTION: Substitutes for Modified Starches
TITLE OF INVENTION: Latexes in Paper Manufacture
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TITLE OF INVENTION: Glucan-containing Compositions and
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FILING DATE: 1998-01-16
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19; Conservative
                                             FastSEQ for Windows Version 3.0
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86.4%; Pred. No. 1e-07;
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; TYPE: PRT ; ORGANISM: streptococcus mutans US-09-740-274-4
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US-09-007-999-2
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                                                                                                                                             CURRENT FILING DATE: 1998-12-11

EARLIER APPLICATION NUMBER: 09/007,999

EARLIER FILING DATE: 1998-01-16

EARLIER FILING DATE: 1998-01-16

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER APPLICATION NUMBER: 09/009,620

EARLIER APPLICATION NUMBER: 09/009,620

EARLIER APPLICATION NUMBER: 08/485,243

EARLIER APPLICATION NUMBER: 09/008,172

EARLIER FILING DATE: 1995-06-07

EARLIER APPLICATION NUMBER: 09/008,172

EARLIER APPLICATION NUMBER: 08/482,711

EARLIER APPLICATION NUMBER: 08/482,711

EARLIER APPLICATION NUMBER: 08/482,711

EARLIER PILING DATE: 1998-01-06-07

NUMBER: 09 SEO ITD NOS-06-07
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Best Local Similarity 86.4
Matches 19; Conservative
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LENGTH: 1475
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Patent No. 6087559
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                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
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TITLE OF INVENTION: Substitutes for Modified Starch and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0356D
CURRENT APPLICATION NUMBER: US/09/007,999
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
ORGANISM: Streptococcus mutans
-09-210-361-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
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                                           LENGTH: 1475
TYPE: PRT
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86.4%; Pred. No.
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1.6e-07;
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-740-274-2
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US-09-740-274-2
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US-09-604-957-5
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
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Best Local Similarity 86.4
19; Conservative
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Patent No. 6465203
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                                                                   SEQ ID NO 5
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TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
CURRENT FILING DATE: 2000-06-18
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TYPE: PRT
ORGANISM: Leuconostoc mesenteroides
09-604-957-5
                                                                                                PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
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                                                                                     SOFTWARE: PatentIn Ver. 2.1
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                                  LENGTH: 523
TYPE: PRT
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ITLE OF INVENTION: Glucan-containing Compositions and Paper
ILE REFERENCE: 0357CRD
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FILING DATE: 1998-01-20
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LEER, ROBERT-JAN
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Pred. No. 1.6e-07;
1; Mismatches 2;

    Mismatches

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Pred. No. 1.6e-07
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TYPE: PRT
; ORGANISM: Lactobacillus reuteri
US-09-604-957-7
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; TYPE: PRT
; ORGANISM: Lactobacillus reuteri
US-09-604-957-3
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US-09-604-957-3
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CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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Patent No. 6486314
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Best Local &
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Best Local Similarity
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APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
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Patent No. 6486314
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                                                              Matches
                                                                                           Query Match
                                                                              Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
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APPLICANT: DIJKHUIZEN, LUBBERT
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 620 IPNYSFVRAHDNNSQDQIQNAIRDV 644
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                         1 VPSYSFARAHDS----EVQDIIRDI 21
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LEER, ROBERT-JAN
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48.0%;
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Pred. No. 0.0033;
7; Mismatches
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Pred. No.
                                                           Score 68; DB 4;
Pred. No. 0.0093;
7; Mismatches
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RESULT 10
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US-09-008-172-2
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APPLICANT: WELSH, Thomas
APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
FILE REFERENCE: 147-195P
CURRENT APPLICATION NUMBER: US/09/499,203
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VAN GEBL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
                                                                                       Sequence 2, Application US/09008172
Patent No. 6127602
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 4
LENGTH: 545
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Patent No. 6486314
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                                                                                                                                                                                                                                                                                                                                          Query Match
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starch and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0356D
CURRENT APPLICATION NUMBER: US/09/008,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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12; Conservative
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Pred. No. 0.016;
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Pred. No. 0.016;
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Best Local Similarity
Matches 13; Conserva
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CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 09/009,620
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LENGTH: 1430
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EARLIER SPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 08/485,243
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEO ID NOS: 6
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                 CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
                                                                                      APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions
FILE REFERENCE: 0357CRD TO 100.774
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hes 13; Conserv
APPLICATION NUMBER:
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Substitutes for Modified Starches and
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Pred. No. 0.
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Pred. No. 0.
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0.049;
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; MOLECULE TYPE: p
; ORIGINAL SOURCE:
; ORGANISM: Stre
US-08-793-824-2
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US-08-793-824-2
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SEQ ID NO 6
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                                                                                                    TELEX: 26547
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1577 amino acids
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                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PM76.
FILING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                             TOPOLOGY:
                                                                         STRANDEDNESS:
                                                                                         TYPE: amino acid
                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Level B, 168 Walker Street
NO. 5981838th Sydney
New South Wales
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61 2 957 6288
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Giffard,
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              Streptococcus salivarius
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Philip Morrison
Nicholas Anthony
Genetic Manipulation of Plants to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Increase Stored Carbohydrates
                                                                                                                                                                                                                              AU PM7643
                                                                                                                                                                                                                                                                                    US/08/793,824
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Pred. No. 0.049;
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; TYPE: PRT ; ORGANISM: Leuconostoc mesenteroides US-09-604-957-6
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                                                                                                                              ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4115
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-134-001C-4115
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
                                                                                                                                                                         NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4115
LENGTH: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
---- Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 584
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APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4115, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6486314
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                                                               Matches
                                                                                            Query Match
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 00201871.1 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn Dougette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/604,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388
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                                                                                                                                                                TYPE: PRT
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 210 VPTYNFAVAVDDHYMQISDVIR 231
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                                                               10;
                                                                                  Similarity
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                              VPSYSFARA---HDSEVQDIIR 19
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RAHAOUI, HAKIM
LEER, ROBERT-JAN
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                                                               Conservative
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Pred. No. 0.05
4; Mismatches
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Pred. No. 0.025;
                                                                                Score 46.5;
Pred. No. 1
                                                                  Mismatches
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US-09-345-473E-37

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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-345-473E-37
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Best Local Similarity
Matches 8; Conservi
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                                             US-08-913-578-2
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SOFTWARE: FRSUSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 309
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APPLICANT: HOdge, Martin
TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2,
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/09345473E Patent No. 6558903
Best Local Similarity
                Query Match
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                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9601069.9
APPLICATION TO 196
FILING DATE: 19-AN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6218159el tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406-0939
COMPUTER READABLE FORM:
                                                            MOLECULE TYPE:
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 709 Security: King of Prussia
                                                                            TOPOLOGY:
                                                                                       STRANDEDNESS:
                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/913,578 FILING DATE: 17-JAN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190
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                                                                                                                         484 amino acids
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41.4%;
40.9%;
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Pred. No.
                                                                                                                                                                                                                                    P31352
Score 45.5;
Pred. No. 16;
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                 DB 3;
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                Length 484;
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RESULT 19
US-08-785-427-2
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US-09-107-532A-4217
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                                                                                                                    Sequence 4217, Application US/09107532A
Patent No. 6583275
                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASCSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,427
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                       GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 9601
FILING DATE: 19-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                            NUMBER OF SEQUENCES:
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9; Conserv
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STREET: 100 Beaver Street
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Pred. No. 1
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                                                           and David Bush AND AMINO ACID SEQUENCES RELATING TO FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
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RESULT 21
US-08-751-189-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harringtor APPLICANT: Robinson,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 15-NOV-1996
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...565
SEQUENCE DESCRIPTION: SEQ ID NO: 4217:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 PSLAFVATHDIELTEILKN 498
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                                                                                                                                                    91320-1789
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REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                           Harrington, Lea A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.8%;
                                                                                                                                                                                                                                                                                                                      No. 5919656el Genes Encoding Telomerase Protein
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                 US/08/751,189
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                                                          Version #1.30
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Query Match
Best Local Similarity
Matches 7; Conserve
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Patent No. 5981
                                 Matches
                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
;-09-060-836-3
                                                              Query Match
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NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-4
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
PILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harrington, AppLICANT: Robinson, MuTITLE OF INVENTION: No. TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: unl
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                                                                                                                                            STRANDEDNESS:
                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 91320-1789
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                                                                                                                                                                            ENGTH:
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   1 VPSYSFARAHDSEVQDI 17
                                 Similarity 41.7 7; Conservative
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                                               39.1%;
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Murray O.
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Pred. No.
                               Score 43; DB 2; ___
Pred. No. 3.2e+02;
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205 MPSYSLSLGEREEVEDL 221

RESULT 23 US-09-184-445-3

Sequence 3, Application US/09184445
Patent No. 6174703

GENERAL INFORMATION:

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; MOLECULE TYPE: protein US-09-184-445-3
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ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2627 amino acids
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APPLICANT: Benezr
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
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                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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Local Similarity 41.2%;
nes 7; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                      STREET:
                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    205 MPSYSISIGEEEEVEDI 221
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1840 De Havilland Drive
                                                                                                                                                                                      E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                   Benezra,
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Pred. No. 3.2e+02
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                                                             US-08-684-024-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 391-0526 INFORMATION FOR SEQ ID NO: :
Matches
               Best Local
                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Benezr
                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match
Local Similarity 46.7%;
hes 7; Conservative
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NAME: White, John P.
28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BNGTH:
                                                                                               TOPOLOGY:
                                                                                                         STRANDEDNESS: single
                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                          ENGTH:
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Similarity 7; Conserv
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                  38.2%;
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Pred. No.
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                                                                                                                                                                                                                                           1747/46621-A
                Score 42; DB 2;
Pred. No. 21;
      Mismatches
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                                   Length 196;
        Indels
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          Gaps
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KTHDDELKDYIRKIL 63

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RESULT 26
US-09-145-868-2
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US-09-145-868-9
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Patent No. 6096522
GENERAL INFORMATION:
APPLICANT: Benezra, Robert
                                                                                                                                                                                                                                                                               Sequence 9, Application US/09145868 Patent No. 6096522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Benezro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,868
FILING DATE: 02-SEP-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENE ENCODING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
            COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                             APPLICANT: Benezra, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                  ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                           49
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                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
PatentIn Release #1.0, Version #1.30
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) 391-0526
NO: 2:
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                                                                                                                                                                                                                                                    Robert
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Pred. No. 21;
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RESULT 29 US-08-557-309B-37

Sequence 37, Appli Patent No. 5916572

Application US/08557309B

GENERAL INFORMATION:

APPLICANT: APPLICANT:

Skeiky, Yasir A.W. Lodes, Michael J. Houghton, Raymond L.

Reed, Steven G.

APPLICANT:

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                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/424,978B CURRENT FILING DATE: 1999-12-02 PRIOR APPLICATION NUMBER: US 60/048,771 PRIOR FILING DATE: 1997-06-06 NUMBER OF SEQ ID NOS: 43 SOPTWARE: Patentin version 3.1 SEQ ID NO 39 SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.2%;
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/09424978B Patent No. 6664445
                                                                  Query Match
Best Local Similarity 30.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Falco, Saverio Carl
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Thorpe, Catherine J.
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REFERENCE: BB-1087
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                               TYPE: PRT
ORGANISM: Gylcine max
                                                                                                                                                                                                    LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acid
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 17-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
 321 VDTYGTGKIHDKEILNIVKE 340
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                  1 VPSYSFARAHDSEVQDIIRD 20
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                                                                         7; Mismatches
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Pred. No. 21;
                                                                                         Score 42; DB
Pred. No. 49;
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RESULT 30
US-08-834-306-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/557,309B FILING DATE: 14-NOV-1995 CLASSIFICATION: 435 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Maki, David J. REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 210121.422 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CO
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 639 amino acid
                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                        STREET: OUTTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 37.3%;
Local Similarity 47.1%;
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington
                                                                         APPLICATION NUMBER: US/08/834,306 FILING DATE: 15-APR-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C1
                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479
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                                                                                                                                                                                                                                                                                                      Washington
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Pred. No. 1.3e+02;
Pred. No. 1.3e+02;
Niematches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                    701 Fifth Avenue
                                                                                                                                                                Version
                                                                                                                                                                #1.30
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Search completed: May 4, 2004, 09:14:13 Job time : 15 secs
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US-08-834-306-37
                                                                                                                                 Matches
                                                                                                                                             Query Match 37.3%;
Best Local Similarity 47.1%;
                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                               STRANDEDNESS:
                                                                 479 VPGWSEALLHDAEFQQL 495
                                                                                                 1 VPSYSFARAHDSEVQDI 17
                                                                                                                                 8
                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                              639 amino acids
                                                                                                                                 Conservative
                                                                                                                                                                                                                linear
                                                                                                                                 ů,
                                                                                                                                                  Score 41; DB 3;
Pred. No. 1.3e+02;
                                                                                                                                 Mismatches
                                                                                                                                                               Length 639;
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Minimum
Maximum
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No.
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Perfect score;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on:
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB seq
                                                                                                                                                                                                                                                      Score
    Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

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RESULT 2
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 09/09,620
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR FILING DATE: 1995-06-07
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                                                                                                                                       Sequence 2, Application US/09740274
Patent No. US20020031826A1
GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-contai
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PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/482,711
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 4
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 FILE REFERENCE: 0357CRD
CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
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TITLE OF INVENTION: Glucan-co
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TYPE: PRT
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US-10-425-114-71916

US-10-425-114-71922

US-10-425-114-71923

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US-10-425-114-71954

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; Sequence 13, Application US/09995749A
; Patent No. US20020155568A1
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FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILLING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
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PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 09/485,243
PRIOR APPLICATION NUMBER: 09/485,243
PRIOR PRILING DATE: 1995-06-07
PRIOR PRILING DATE: 1995-06-07
PRIOR PRILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR PRILING DATE: 1995-06-07
PRIOR PRILING DATE: 1995-06-07
NUMBER: 05/482,711
PRIOR FILING DATE: 1995-06-07
NUMBER: 05/482,711
PRIOR FILING DATE: 1995-06-07
NUMBER: 05/482,711
GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDR
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
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SEQ ID NO 11
LENGTH: 522
TYPE: PRT
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APPLICANT: DIJKHUIZEN, LUBBEI
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
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86.4%; Pred. No.
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                                                                                                                         GERRITDINA HENDRIKA
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Patent No. US20020155568A1
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LENGTH: 535
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              CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
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PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
                                                                                                                                       TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES FILE REFERENCE: BO43388-CIP
                                                                                                                                                                               APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
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APPLICANT: DIJKHUIZEN, LUBBERT
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PRIOR FILING DATE: 2000-06-28
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FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
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APPLICANT: DIJIKUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKEN
APPLICANT: LEER, ROBERT-JAN
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BENERAL INFORMATION:
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PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
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TYPE: PRT
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SEQ ID NOS: 19
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Pred. No. 0.013;
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Pred. No. 0.015;
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                                  PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 545
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Patent No. US20020155568A1
GENERAL INFORMATION:
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Publication No. US20030229923A1
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                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
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CURRENT APPLICATION NUMBER: US/10/417,280A
CURRENT FILING DATE: 2003-04-15
FRIOR APPLICATION NUMBER: DE 19905069.4
PRIOR PILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: US 09/499,203
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
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SOFTWARE: PatentIn version 3.2
                                                                                                                           PRIOR APPLICATION NUMBER: EPO 00201871.1
                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES FILE REFERENCE: BO43388-CIP
                                                                                                                                                                                                                                                                       APPLICANT: VAN GEBL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
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                   LENGTH: 54
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ORGANISM: Streptococcus mutans
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QUANZ, Martin
KNUTH, Karola
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RAHAOUI, HAKIM
LEER, ROBERT-JAN
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Pred. No. 0.066;
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Pred. No. 0.055;
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US-09-995-749A-10

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SEQ ID NO 6
LENGTH: 1430
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: "Thomas J
APPLICANT: Kovalic David K
                                                               SEQ ID NO 168435
LENGTH: 117
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Best Local
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Patent No. US20020031826A1
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                                                                                             APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER: OF SEQ ID NOS: 285684
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PRIOR FILING DATE: 1998-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
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CURRENT FILING DATE: 2000-12-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Glucan-containing Compositions and Paper
            ORGANISM: Glycine max FEATURE:
NAME/KEY: unsure
                                                 TYPE: PRT
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APPLICATION NUMBER:
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FILING DATE: 1995-06-07
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NUMBER: 08/482,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1995-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 9;
Pred. No. 0.063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2;
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PRIOR ADDITION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-16
PRIOR PELLING DATE: 2001-02-16
PRIOR PELLING DATE: 2001-02-16
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PRIOR PELLING DATE: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-282-122A-71700
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Query Match 44.1%;
Best Local Similarity 45.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILLING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (11)...(11)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                       LENGTH: 465
TYPE: PRT
ORGANISM: Staphylococcus haemolyticus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SYSFARAHDSEVQDIIRDII 22
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Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind, Judith
Wall, Daniel
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Score 48.5; I
Pred. No. 19;
5; Mismatches
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See File Wrapper or PALM
                                                                       DB 12;
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                                                                       Length 465;
           Indels
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           Gaps
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEM.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRICING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/23,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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US-09-815-242-5584
                                                                                                                                                                                                                                                                                                                                                        Sequence 12456, Application Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                            APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-16
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               CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind, Judith W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                               Application US/09815242
NUMBER:
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Pred. No. 3
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RESULT 15
US-10-424-599-194106
; Sequence 194106, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic David K
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; LENGTH: 487
; TYPE: PRT
; ORCANISM: Staphylococcus aureus
US-09-815-242-12456
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 264904, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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APPLICANT: Kovalic David K
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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LOCATION: (1)..(166)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_81228C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
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tes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/206,848
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Pred. No.
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Pred. No. 30;
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                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/253,625
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Best Local
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
                                                                                      PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
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                                                                                                                                        PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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LOCATION: (1)..(963)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Zyskind, Judith
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Malone, Cheryl
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ilarity 42.9%;
Conservative
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dio, Carlos
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Pred. No.
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Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 203-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 267457

LENGTH: 115

TYPE: PRT

ORCANTT
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US-10-424-599-267457
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                                         ; ORGANISM: Homo
US-09-862-027-37
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                                                                                        SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 309
                                                                                                                                                                                                                                                                   Sequence 37, Application U Patent No. US20020142428A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                 APPLICANT: Hodge, Martin R.

TITLE OF INVENTION: No. U820020142428A1el Kinases and Uses Thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(115)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                           TYPE: PRT
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41.8%;
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Pred. No.
 Score
Pred.
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Pred. No. 4
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 DB 9;
31;
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; ORGANISM: Homo sapiens US-10-131-410-117
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US-10-131-410-117
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US-10-276-774-2103
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                                                                                         Query Match
Best Local :
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SEQ ID NO 117
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SOFTWARE: Custom
SEQ ID NO 2103
LENGTH: 490
TYPE: PRT
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APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
TITLE OF INVENTION: TUMORS
FILE REFERENCE: SCH-1763
CURRENT APPLICATION NUMBER: US/10/131,410
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 09/646,673
PRIOR FILING DATE: 2000-09-20
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Publication No.
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Publication No. US20040053245A1
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/DE99/00908
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 202
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2000-04-27
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CURRENT FILING DATE: 2002-11-18
                                                                                                                                                                              TYPE: PRT
                                                             41.8%;
Local Similarity 36.4%;
les 8; Conservation
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            1 VPSYSFARAHDSEVQDIIRDII 22
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SCHMITT, ARMIN
PILARSKY, CHRISTIAN
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D. US20030235915A1
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                                                                  6; Mismatches
                                                                                     Score 46;
Pred. No.
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RESULT 23
US-10-433-794-17
; Sequence 17, Application US/10433794
; Publication No. US20040077044A1
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Best Local Similarity
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US-10-131-410-180
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SEQ ID NO 49
LENGTH: 779
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Publication No. US20030175288A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 202
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 180
LENGTH: 564
TYPE: PRT
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TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
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PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
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CURRENT APPLICATION NUMBER: US/10/131,410
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 09/646,673
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: PCT/DE99/00908
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
TITLE OF INVENTION: TUMORS
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8; Conserv
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SCHMITT, ARMIN
PILARSKY, CHRISTIAN
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larity 44.4%;
Conservative
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                                                                                                                                                                                                                       DB 14;
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                                                                                                                                                                                                                     Length 779;
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RESULT 24
US-10-282-122A-43803
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APPLICANT: Wang, Lia
APPLICANT: Zamudio
APPLICANT: Malone,
                                                                                                                                                                                                                                                                   Sequence 43803, Application US/10282122A
Publication No. US20040029129A1
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Best Local :
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SEQ ID NO 17
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APPLICANT: LU, Yan, HAFALIA, April J.A.;
APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
APPLICANT: ARVIZU, Chandra S.; FORSYTHE, Ian J
TITLE OF INVENTION: KINASES AND PHOSPHATASES
FILE REFERENCE: PI-0311 USN
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CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: PCT/US01/47431
PRIOR FILING DATE: 2001-12-04
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PRIOR APPLICATION NUMBER: US 60/251,814
PRIOR FILING DATE: 2000-12-07
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NAME/KEY: misc_feature
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nes 8; Conservative
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    INVENTION: Identification
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                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                  Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                       Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                            Wall, Daniel
Trawick, John
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US-10-424-599-232822
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US-10-424-599-232822
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 222822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 232822, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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SEQ ID NO 43803
LENGTH: 484
                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
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APPLICANT: Kovalic David K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR ETILING DATE: 2000-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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                                                                                                                                                                                                                                                                                    LENGTH: 54
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Local Similarity 40.9%;
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10 VSSYSLARAHD
                                       1 VPSYSFARAHD 11
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                                                                                    Conservative
                                                                                                      40.9%;
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                                                                                    Score 45; DB Pred. No. 5.9; 0; Mismatches
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Pred. No. 6
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RESULT 28
US-10-424-599-199858
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Best Local Similarity
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US-10-424-599-184218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49229C.1.pep
US-10-424-599-229462
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GENERAL INFORMATION
              Sequence 199858, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 184218
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Best Local
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SEQ ID NO 229462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
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ORGANISM: Glycine max
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OTHER INFORMATION: unsure at all Xaa locations
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Similarity 44.0%;
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Pred. No.
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Pred. No.
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               RESULT 30
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US-09-895-828-454
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US-10-114-666-454
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LENGTH: 174
TYPE: PRT
ORGANISM: Glycine "
                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.539
CURRENT APPLICATION NUMBER: US/09/895,828
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 473
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 454
LENGTH: 255
TYPE: PRT
                                                                                                                                              Query Match 40.9%;
Best Local Similarity 38.1%;
Matches 8; Conservative
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APPLICANT:
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Best Local Similarity 40.0%;
Matches 8; Conservative
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APPLICANT: McNe.
APPLICANT: Wata
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules.
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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NAME/KEY: unsure
LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                     148 VPSYMKSRLTYNQINDVIKEI 168
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                                                                                                             VPSYSFARAHDSEVQDIIRDI 21
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McNeill, Patricia D
Watanabe, Yoshihiro
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Pred. No.
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Pred. No.
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Sequence 454, Application US/10114666
Publication NO. US20030103994A1
GENERAL INFORMATION:
APPLICANT: Watanabe, Yoshihiro

APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

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FILE REPERENCE: 210121.539C1
CURRENT APPLICATION NUMBER: US/10/114,666
CURRENT APPLICATION NUMBER: US/10/114,666
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 479
SOFTWARE: FAST
LENGTH: 255
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-666-454
Query Match
Best Local Similarity 38.1%; Pred. No. 36;
Best Local Similarity 38.1%; Pred. No. 36;
Best Local Similarity 7; Mismatches 6; Indels 0; Gaps
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps
Oy
1 VPSYSFARAHDSEVQDITRDI 21
Db 148 VPSYMKSRLTYNQINDVIKEI 168
Search completed: May 4, 2004, 09:25:42
Job time: 35.3333 secs
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